

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	218	5.4	2433	4	US-09-300-958A-24		Sequence 24, Appl
2	215.2	5.4	4157	4	US-08-556-422A-1		Sequence 1, Appl
3	94.2	2.4	3524	4	US-09-077-940A-3		Sequence 3, Appl
4	79.2	2.0	3692	4	US-09-077-940A-1		Sequence 1, Appl
5	72.6	1.8	3288	2	US-08-620-694A-1		Sequence 1, Appl
6	72.6	1.8	3288	3	US-09-022-255-1		Sequence 1, Appl
7	72.6	1.8	3288	3	US-09-022-696-1		Sequence 1, Appl
8	72.6	1.8	3288	3	US-08-978-773-1		Sequence 1, Appl
9	72.6	1.8	3288	3	US-09-022-253-1		Sequence 1, Appl
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11	72.6	1.8	3288	3	US-09-022-259-1		Sequence 1, Appl
12	72.6	1.8	3288	3	US-09-022-257-1		Sequence 1, Appl
C	13	67.4	1.7	3358	3	US-08-957-063-4	Sequence 4, Appl
	14	67.4	1.7	3358	4	US-09-487-685-4	Sequence 4, Appl
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	16	66.6	1.7	2854	1	US-08-121-713D-57	Sequence 57, Appl
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18	66.6	1.7	2854	2	US-09-060-692-57	Sequence 57, Appl	
19	66.6	1.7	2854	3	US-08-833-391-57	Sequence 57, Appl	
20	66.6	1.7	2854	4	US-09-060-610-57	Sequence 57, Appl	
21	66.6	1.7	2854	5	PCF-US94-10151A-57	Sequence 57, Appl	
22	66.4	1.7	3757	2	US-09-016-366A-13	Sequence 13, Appl	
23	66.4	1.7	3757	3	US-08-978-404B-19	Sequence 19, Appl	
C	24	66.4	1.7	80246	2	US-09-078-294-4	Sequence 4, Appl
	25	65.4	1.6	35828	4	US-09-449-218D-17	Sequence 17, Appl
26	65.4	1.6	35828	4	US-09-668-529A-17	Sequence 17, Appl	
27	65.4	1.6	35828	4	US-09-668-037A-17	Sequence 17, Appl	

Qy	547	GATGTGTCCAGTTTTCACGACGGTTGAA-----AGACTTTGAGACGGCG	588
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Qy	649	CTCTACACCGCCACTGTGAAGAACTTCCTGGGACTGAGCCCATCATCTCCGAGCTGTG	708
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Qy	709	GGTCGAGCTGAGGACTGGATTTCGAACAGAGACCTTTCATCCTGGCTTAATGTCCAGCC	768
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Qy	949	TGGACGACGTTCTGAAGGCTGACCTGCTGCGCCAGGGCCGACGAGATGCGCGGCTCC	1008
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[illegible]

Query Match	5.48;	Score 215.2;	DB.4;	Length 4157;
Best Local Similarity	48.9%;	Pred. No. 2.4e-45;		
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Db	223	GACATCTACAACATACTCAGCCTTGCTGCTGAGCGAGGACAAGGACACCTTGTACATAGGT	282	
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; Patent NO. 6576441
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru et al.
; TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE SAME
; FILE REFERENCE: 0020-4426P
; CURRENT APPLICATION NUMBER: US/09/077,940A
; CURRENT FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3524
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(38)
; OTHER INFORMATION:
; NAME/KEY: 3'UTR
; LOCATION: (2706)..(3524)
; OTHER INFORMATION:
; NAME/KEY: CDS
; LOCATION: (39)..(2702)
; OTHER INFORMATION:
; US-09-077-940A-3

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RESULT 3
US-09-077-940A-3
; Sequence 3, Application US/09077940A

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 25, 2003, 17:51:04 ; Search time 983.19 Seconds
(without alignments)
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4008	100.0	4008	19	AAV07279 Rat semaphorin W e
2	3122.2	77.9	4024	21	AA287977 Mouse semaphorin W
3	2331	58.2	2331	19	AAV07280 Rat semaphorin W e
4	1875.2	46.8	2971	22	AAF93776 Human cDNA encodin
5	1673.6	41.8	2893	20	AAV07281 DNA encoding SBSEM
6	1673.6	41.8	2894	20	AAV07282 EST sequence for D
7	1404.2	35.0	2315	19	AAV07281 Human semaphorin W
8	1391.2	34.7	1761	19	AAV07282 Human semaphorin W

9	654	16.3	799	20	AAV07283	EST sequence for D
10	597.8	14.9	928	25	ABT32087	NOVX DNA sequence
11	527.4	13.2	777	25	ABT32088	NOVX DNA sequence
12	505.2	12.6	671	24	ABL89791	Human polynucleoti
13	408	10.2	669	22	AAF93972	Primer specific fo
14	251.8	6.3	3293	22	AAV08048	Human extracellular
15	248.6	6.2	2155	22	AAV08048	Human SEC6 nucleic
16	248.6	6.2	2156	22	AAV08048	Human SEC6 nucleic
17	248.6	6.2	2284	22	AAV08048	Human SEC7 nucleic
18	248.6	6.2	3556	22	AAV08048	Human secreted pro
19	248.6	6.2	3776	24	ABN83983	Human gene sequenc
20	247.8	6.2	2558	24	AAV08048	Human gene sequenc
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23	247	6.2	3781	22	AAV07092	Human PRO1480 (UNQ
24	247	6.2	3781	22	AAV07092	Primer #75 used in
25	247	6.2	3781	25	AAV07092	Human PRO1480 cDNA
26	247	6.2	3781	25	ABX98379	Human cDNA encodin
27	247	6.2	3781	25	ABX98881	Novel human secret
28	247	6.2	3781	25	ACA05926	Human secreted/tra
29	247	6.2	3781	25	ABX97970	Human PRO polynucl
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34	246	6.1	3868	24	AAV08947	Human cDNA encodin
35	245.4	6.1	3503	22	AAF29461	Murine M-Sema-F CD
36	245.4	6.1	3766	24	ABV77918	Human MOL5a cDNA.
37	245.4	6.1	3766	24	ABN83984	Hypoxia-induced pr
38	245.4	6.1	3766	25	ACC51059	Human gene sequenc
39	245.4	6.1	3766	25	ABX76369	Human bladder canc
40	238.4	5.9	8095	24	ABX92031	Lung cancer-associ
41	238.4	5.9	8144	25	ABT13397	Lung specific nucl
42	238.2	5.9	2703	21	AAA47437	Breast specific re
43	238	5.9	333	19	AAV07286	Sequence encoding
44	228	5.7	2390	24	ABQ11109	Human semaphorin W
45	224.4	5.6	2615	24	ABQ99272	DNA encoding human
						Human coding sequen

ALIGNMENTS

RESULT 1

AAV07279

ID AAV07279 standard; cDNA to mRNA; 4008 BP.

XX AAV07279;

AC AAV07279;

XX 08-SEP-1998 (first entry)

DT Rat semaphorin W encoding cDNA with 5'UTR and 3'UTR.

DE Rat semaphorin W; nerve extension inhibitor; antiallergic; anticancer;

XX Immunosuppressant; gene therapy; diagnosis; research reagent; ds.

KW Rattus norvegicus.

XX Key Location/Qualifiers

PH 5'UTR 1..75

FT /*tag= a

FT CDS 76..2406

FT /*tag= b

FT /*product= "semaphorin W"

FT 5'UTR 2407..3977

FT /*tag= c

FT polyA_signal 3978..4008

FT /*tag= d

XX WO9815628-A1.

XX 16-APR-1998.

PD 03-OCT-1997; 97WO-JP03549.

XX

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XX 09-OCT-1996; 96JP-0287636.
XX (SUMU) SUMITOMO PHARM CO LTD.
XX Kikuchi K, Kimura T;
XX WPI; 1998-261015/23.
XX P-PSDB; AAW51313.
XX Nerve extension inhibitor protein semaphorin W - is useful as
XX therapeutic drug and diagnostic and research reagent
XX Claim 2; Page 55-57; 90pp; Japanese.
XX The present sequence encodes rat semaphorin W. Semaphorin W and its
XX derivatives are nerve extension inhibitors which are useful as
XX anti-allergic, immunosuppressant and anticancer agents. The DNA
XX encoding semaphorin W can also be used in gene therapy, e.g. using
XX a viral vector. The proteins, peptides, DNA and antibodies which
XX recognise the protein or peptides, can be used as diagnostic or
XX research reagents. Semaphorin W can be used as a screen for
XX semaphorin W antagonists with possible therapeutic use.
XX Sequence 4008 BP; 775 A; 1135 C; 1141 G; 957 T; 0 other;
XX
XX Query Match 100.0%; Score 4008; DB 19; Length 4008;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 4008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GCCGAGGCGCGCAGTAGCGGTACTAAGTAGAGGCTGCTGGACGCGCGCCGCCCGCGCT 60
QY 61 CAGGCGGACAGAGATGCTTCCAGGCGCGAGCGCGCGCGCGCGCGCGCGCGCT 120
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DB 841 TTCACGAGACCTCCGAGCTGTGGACTCTATGAGCGCATCAAGTCCCAAGAGTGGCC 900
QY 901 CGAGTGTGCGGGGAGACCTTGGGGCAGAGACCTTTCACAGAGATGGAGAGCTTT 960
DB 901 CGAGTGTGCGGGGAGACCTTGGGGCAGAGACCTTTCACAGAGATGGAGAGCTTT 960
QY 961 CTGAAGGCTGACCTGCTGTGCCAGGCGCGGAGCATGGCCGGGCTTCTGCAG 1020
DB 961 CTGAAGGCTGACCTGCTGTGCCAGGCGCGGAGCATGGCCGGGCTTCTGCAG 1020
QY 1021 GCTATGGCAGAGCTTTCGGCTCAGCTTGAGCGGGAACCCCATCTTTTATGGGATCTTT 1080
DB 1021 GCTATGGCAGAGCTTTCGGCTCAGCTTGAGCGGGAACCCCATCTTTTATGGGATCTTT 1080
QY 1081 TCCTCCAGTGGGAGGAGCTGCCATCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
DB 1081 TCCTCCAGTGGGAGGAGCTGCCATCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
QY 1141 CGGGCAGTGTGAATGGTCCCTTTAGAGAGCTTAAACATGACTGCAACAGGGAGCTGCT 1200
DB 1141 CGGGCAGTGTGAATGGTCCCTTTAGAGAGCTTAAACATGACTGCAACAGGGAGCTGCT 1200
QY 1201 GTCATGTGCAACAGAGTGTGCCAGCCAGACCTGGAGAGTGTGATGCAACAAACATGAAG 1260
DB 1201 GTCATGTGCAACAGAGTGTGCCAGCCAGACCTGGAGAGTGTGATGCAACAAACATGAAG 1260
QY 1261 CTCACAGAGTGTGATTCCTACTCTCCCTGCCAGACCGGGTGTCTACCTTTATCAGAGAC 1320
DB 1261 CTCACAGAGTGTGATTCCTACTCTCCCTGCCAGACCGGGTGTCTACCTTTATCAGAGAC 1320
QY 1321 CACCTCTCATGAGCAGGCGCTGTTCGGGCTGAGCGCGCCCTGCTGTGTCTACTACA 1380
DB 1321 CACCTCTCATGAGCAGGCGCTGTTCGGGCTGAGCGCGCCCTGCTGTGTCTACTACA 1380
QY 1381 GATACAGCTTATCTCAGAGTGTGCGCCACAGGGTGTGACAGCTCTCTCAGGGAAAGATAT 1440
DB 1381 GATACAGCTTATCTCAGAGTGTGCGCCACAGGGTGTGACAGCTCTCTCAGGGAAAGATAT 1440
QY 1441 GACGTGTCTACCTGGGACAGAGATGACACTTCCACCGGGGTGTGGGATTTGGAGCT 1500
DB 1441 GACGTGTCTACCTGGGACAGAGATGACACTTCCACCGGGGTGTGGGATTTGGAGCT 1500
QY 1501 CAGCTCAGTGTCTGGAGATCTGCGCTTGTTCACAGAACACACCGGTTGAGAGCATG 1560
DB 1501 CAGCTCAGTGTCTGGAGATCTGCGCTTGTTCACAGAACACACCGGTTGAGAGCATG 1560
QY 1561 AAATTTGTACACAGATTTGCTCTGTGGGCTCCCATCTGAGGTGACAAAGTGAACACC 1620
DB 1561 AAATTTGTACACAGATTTGCTCTGTGGGCTCCCATCTGAGGTGACAAAGTGAACACC 1620
QY 1621 AGCAACTGTGGCGCTCTCCAGAGTGTCTCGGAGTGTATCTTGGCCAGAGACCCGTGTGC 1680
DB 1621 AGCAACTGTGGCGCTCTCCAGAGTGTCTCGGAGTGTATCTTGGCCAGAGACCCGTGTGC 1680
QY 1681 GCCTGGAGCTTCCGGCTTGTGTGTGGCCAGCGGAGCAGCAGCGGGATGTT 1740
DB 1681 GCCTGGAGCTTCCGGCTTGTGTGTGGCCAGCGGAGCAGCAGCGGGATGTT 1740

Db 721 GCTGAGTGGGGGATGAAGATGGAGACGATGAATCTTTTCTTACGGAGACCTCC 780
 QY 856 CGAGTGTGGACTCCCTATGAGCGCATCAAGGTCCCAAGAGTGCCTGAGTGTGTGGGGG 915
 Db 781 CGAGTGTGGACTCCCTATGAGCGCATCAAGGTCCCAAGAGTGCCTGAGTGTGTGGGGG 840
 QY 916 GACCTTGGGGGCGAGGAGACCCCTTACGAGAGATGAGACGCTTTCTGAAGGCTGACCTG 975
 Db 841 GACCTTGGGGGCGAGGAGACCCCTTACGAGAGATGAGACGCTTTCTGAAGGCTGACCTG 900
 QY 976 CTGTGCCAGGCGCCGAGCATGCGGGGCTCCGGGCTTCTGAGGCTATGGCAGACTT 1035
 Db 901 CTGTGCCAGGCGCCGAGCATGCGGGGCTCCGGGCTTCTGAGGCTATGGCAGACTT 960
 QY 1036 CGGCTCAGCTGAGCGGGAACCCCATCTTTTATGGGATCTTTTCTCCAGTGGGAA 1095
 Db 961 CGGCTCAGCTGAGCGGGAACCCCATCTTTTATGGGATCTTTTCTCCAGTGGGAA 1020
 QY 1096 GGAGTGCCTATCTGTGTGTGTGCTTCCGACCCCAAGACATPCGGGGCAGTGTCTGAAT 1155
 Db 1021 GGAGTGCCTATCTGTGTGTGTGCTTCCGACCCCAAGACATPCGGGGCAGTGTCTGAAT 1080
 QY 1156 GGTCCCTTTAGAGAGCTAAGACATGACTGCAACAGGGGACTGCTGTCTATGGACAACGAG 1215
 Db 1081 GGTCCCTTTAGAGAGCTAAGACATGACTGCAACAGGGGACTGCTGTCTATGGACAACGAG 1140
 QY 1216 GTGCCCCAGCCAGACCTGGAGAGTGCATCGCAACAAATGAAGCTCCAGCAGTTTGA 1275
 Db 1141 GTGCCCCAGCCAGACCTGGAGAGTGCATCGCAACAAATGAAGCTCCAGCAGTTTGA 1200
 QY 1276 TCCTCACTCTCCCTGCGAGACCGGTGCTCACCTTTATCAGAGACCAACCTCTCATGGAC 1335
 Db 1201 TCCTCACTCTCCCTGCGAGACCGGTGCTCACCTTTATCAGAGACCAACCTCTCATGGAC 1260
 QY 1336 AGGCGCTGTTCCTGGCTGACGGCGCCCTGCTGTCTACTACAGATACAGCCTATCTC 1395
 Db 1261 AGGCGCTGTTCCTGGCTGACGGCGCCCTGCTGTCTACTACAGATACAGCCTATCTC 1320
 QY 1396 AGAGTCTGTGCCCCACAGGGTGACAGCTCTCAGGGGAAAGATATGACGTCTACCTG 1455
 Db 1321 AGAGTCTGTGCCCCACAGGGTGACAGCTCTCAGGGGAAAGATATGACGTCTACCTG 1380
 QY 1456 GGGACAGAGATGACACCTCCACCGGGCTGTGGCAATGGAGCTCAGCTCAGTGTCTG 1515
 Db 1381 GGGACAGAGATGACACCTCCACCGGGCTGTGGCAATGGAGCTCAGCTCAGTGTCTG 1440
 QY 1516 GAGGATCTGCGCTGTTCACAGACACACAGCGGTGAGAGCATGAATTTGTACCAGAT 1575
 Db 1441 GAGGATCTGCGCTGTTCACAGACACACAGCGGTGAGAGCATGAATTTGTACCAGAT 1500
 QY 1576 TGGCTCTGTGGCTCCCATCTAGGTGACACAGTGAACACACAGCAACTGTGGCGCT 1635
 Db 1501 TGGCTCTGTGGCTCCCATCTAGGTGACACAGTGAACACACAGCAACTGTGGCGCT 1560
 QY 1636 CTCAGAGCTGCTCGGAGTGTATCTGTGGCCAGGACCCCGTGTGGCGCTGGAGCTTCCGG 1695
 Db 1561 CTCAGAGCTGCTCGGAGTGTATCTGTGGCCAGGACCCCGTGTGGCGCTGGAGCTTCCGG 1620
 QY 1696 CTTGATGCTTGTGTGGCCACGCGCGGAGACACCGGGGATGGTTCAAGATATAGATCA 1755
 Db 1621 CTTGATGCTTGTGTGGCCACGCGCGGAGACACCGGGGATGGTTCAAGATATAGATCA 1680
 QY 1756 GCGGATCTCTCTTTTGTGTCCAAAAGAACCTGGAGAACATCCCGTGTGTGAAGTT 1815
 Db 1681 GCGGATCTCTCTTTTGTGTCCAAAAGAACCTGGAGAACATCCCGTGTGTGAAGTT 1740
 QY 1816 CCGGTGGCTACTGTGGGCCACGTGGTCTGCCATGTTTCCCGCAGTCTGCTGGGCATCC 1875
 Db 1741 CCGGTGGCTACTGTGGGCCACGTGGTCTGCCATGTTTCCCGCAGTCTGCTGGGCATCC 1800
 QY 1876 TGTGTGTGGACACGCGGAGTGTGAGTGTGCTGCTACTCCCGGAGGATGAGACTAGAG 1935
 Db 1801 TGTGTGTGGACACGCGGAGTGTGAGTGTGCTGCTACTCCCGGAGGATGAGACTAGAG 1860

QY 1936 GTGCTGTGACCCAGGGGCGCATGCGGGCTTATGCTTGCAGTGTTCAGAGGGTGGAGCC 1995
 Db 1861 GTGCTGTGACCCAGGGGCGCATGCGGGCTTATGCTTGCAGTGTTCAGAGGGTGGAGCC 1920
 QY 1996 GCCCGGCTGTGCTGCTTATAGCTTGGTGTGGGGCAGCAGCGGGGACCTCAAAACCG 2055
 Db 1921 GCCCGGCTGTGCTGCTTATAGCTTGGTGTGGGGCAGCAGCGGGGACCTCAAAACCG 1980
 QY 2056 GCCCACACCCCTGTGGGGCTGGATGGTGGCTTTCTCTCGGTGTCTTGAGCATCC 2115
 Db 1981 GCCCACACCCCTGTGGGGCTGGATGGTGGCTTTCTCTCGGTGTCTTGAGCATCC 2040
 QY 2116 CTCACCTCTCTCTGATTGCTCGCGTACGAGCTGCGGCGACAGAGGGAGCTTCTAGCT 2175
 Db 2041 CTCACCTCTCTCTGATTGCTCGCGTACGAGCTGCGGCGACAGAGGGAGCTTCTAGCT 2100
 QY 2176 AGAGACAAGTGGGCTTAGATCTGGGGCTCCACCTTCTGGGACCAAGCTATAGTCAG 2235
 Db 2101 AGAGACAAGTGGGCTTAGATCTGGGGCTCCACCTTCTGGGACCAAGCTATAGTCAG 2160
 QY 2236 GACCCCTCCCTCTCTTCCGCTGAAGATGAACGGCTGCCCTGGCCCTGGGTAAAGCGGGC 2295
 Db 2161 GACCCCTCCCTCTCTTCCGCTGAAGATGAACGGCTGCCCTGGCCCTGGGTAAAGCGGGC 2220
 QY 2296 AGTGGTGTGGTGGCTTCCCTCCACCTTCTCTGCTGATTCTTGCCTCAAGCCAGCCAC 2355
 Db 2221 AGTGGTGTGGTGGCTTCCCTCCACCTTCTCTGCTGATTCTTGCCTCAAGCCAGCCAC 2280
 QY 2356 ATCCGGCTCACTGGGGGCGCTCTAGCCACGCTGTGATGAGACCTCCATCTAA 2406
 Db 2281 ATCCGGCTCACTGGGGGCGCTCTAGCCACGCTGTGATGAGACCTCCATCTAA 2331

RESULT 4

AAF93776
 ID AAF93776 standard; cdna; 2971 BP.

XX AAF93776;

XX 23-MAY-2001 (first entry)

XX Human cDNA encoding a membrane or secretory protein clone PSEC0074.

DE Human; secretory protein; membrane protein; vaccine; gene therapy;
 KW rheumatoid arthritis; diabetes; ss.

XX Homo sapiens.

OS EPI067182-A2.

XX 10-JAN-2001.

XX 07-JUL-2000; 2000EP-0114090.

XX 08-JUL-1999; 99JP-0194179.

XX 11-JAN-2000; 2000JP-0118775.

XX 02-MAY-2000; 2000JP-0183766.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;

XX WPI; 2001-093989/11.

XX P-PSDB; AAB88349.

XX Nucleic acids encoding secretory proteins/membrane proteins, useful in
 PT gene therapy or as candidate target molecules in drug development -

XX Claim 1; SEQ ID 65; 609pp + CD ROM; English.

XX This invention relates to nucleic acid sequences AAF93744 - AAF93916
 CC which encode human secretory or membrane proteins represented by


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Db 1753 CAAGACATAGTCAGCAGATGCTCCTCTTTGTCTTAAGAGCCTCGAGAACGTCCA 1812
Qy 1801 GTAGTGTTCAGTTCGGTGGCTACTGTGGGACAGTGTCTCCATGTTCCCCAGT 1860
Db 1813 GTAGTGTTCAGTTCGGTGGCTACTGTGGGACAGTGTCTCCATGTTCCAAAG 1872
Qy 1861 TCTGCTGGGCATCCTGTGTGTGGCACAGCCAGTGGAGTACTGCGCTCACTCCCGG 1920
Db 1873 TCAGCATGGGCATCCTGTGTGTGGCACAGCCAGTGGAGTACTGCGCTCACTCCCGG 1932
Qy 1921 AGGATGGACTAGAGTGGTGTGACCCAGGCGCATGGGGCTTATGCTTCGAGTGT 1980
Db 1933 CGGATGGACTAGAGTGGTGTGACCCAGGCGCATGGGGCTTATGCTTCGAGTGT 1992
Qy 1981 CAGAGGGTGGAGCCCGCCGCTGTGGCTGTATAGCTGTGGGACAGCCAGCG 2040
Db 1993 CAGAGGGTGGGAGCCCGCCGCTGTGGCTGTATAGCTGTGGGACAGCCAGCG 2052
Qy 2041 GGACCCCTAAACCGGGCCACACCGTTGTGGGGCTGGATTGGTGTCTCTCGGT 2100
Db 2053 GATGCTCCGAGCCGGGCCACAC- --AGTGGGGCGGACTGGCTGCTTCTTGGG 2109
Qy 2101 GTTCTTGACATCCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2160
Db 2110 ATTCTCGCAGCATCCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2169
Qy 2161 AGGAGCTTCTAGTACAGACAAGTGGGCTTAGATCTGGGGCTCCACCTCTCGGACC 2220
Db 2170 AGGGAATCTTGGCTAGAGACAAGTGGGCTTGAGCTGGGGCTCCACCTCTCGGACC 2229
Qy 2221 ACAAGCTATAGTCAGGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2280
Db 2230 ACAAGCTACAGCAAGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2289
Qy 2281 CTGGGTAAAGCGGGAGTGTGTTGGTGGCTTCCCTCCACCTCTCTCTCTCTCTCTCT 2340
Db 2290 CTGGCCAAGAGGGGAGTGTGTTGGTGGATCTCTACACCTCTCTCTCTCTCTCTCT 2349
Qy 2341 CCAAGCCACGCCACATCCGGCTCACTGGGGCGCTCTAGCCACGTGTGTAGACCTCC 2400
Db 2350 CCAAGCCACGCCACATTCGGCTCACTGGGGCGCTCTCTAGCCACGTGTGTAGAACATCC 2409
Qy 2401 ATCTAAGCCGGGAAATGACTGCCAGCCATGAGCAGTCTCTGGAAC 2448
Db 2410 ATCTAGAGTGGGCAATGACCACCTAGTGTATAGTATGATCACTGGGAAC 2457
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RESULT 5

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AAx86126
ID AAx86126 standard; DNA; 2893 BP.
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AC AAx86126;
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XX 15-SEP-1999 (first entry)
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XX DNA encoding SBSEMN1, a semaphorin family polypeptide.
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XX SBSEMN1: semaphorin; neurodegeneration; spinal injury; neuropathy;
KW neuromuscular disorder; muscular dystrophy; psychiatric disorder;
KW inflammatory disorder; developmental malformation;
KW immune system disorder; cancer; viral infection; vaccine; ss.
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XX Homo sapiens.
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XX EP933425-A1.
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XX 04-AUG-1999.
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XX 30-SEP-1998; 98EP-0203287.
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XX 30-JUL-1998; 98GB-0016676.
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PR 30-JAN-1998; 98EP-0300693.
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PR 28-JUL-1998; 98GB-0016423.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
PA Doe TR, Hayes PD, Michalovich D;
PI WPI; 1999-407151/35.
XX P-PSDB; AAY23873.
DR New semaphorin family polypeptide useful for treating spinal injury
PT and muscular dystrophy
XX Claim 7; Page 13-14; 29pp; English.
XX The present sequence encodes SBSEMN1, a semaphorin family polypeptide.
CC The polypeptide may be used to screen for agonists or antagonists
CC including antibodies. Measurement of the level of SBSEMN1 protein
CC and detection of a mutation in its polynucleotide may also be used to
CC diagnose a disease or condition or susceptibility to a disease related
CC to altered expression or activity of SBSEMN1. These diseases and
CC conditions include neurodegeneration, spinal injury, neuropathies,
CC neuromuscular disorders, muscular dystrophy, psychiatric disorders,
CC inflammatory disorders, developmental malformations, disorders of the
CC immune system, cancer and viral infections. The protein may also be
CC used to treat these diseases and conditions by administration as a
CC vaccine.
XX Sequence 2893 BP; 579 A; 825 C; 842 G; 647 T; 0 other;
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Query Match 41.8%; Score 1673.6; DB 20; Length 2893;
Best Local Similarity 82.2%; Pred. No. 0;
Matches 2012; Conservative 0; Mismatches 319; Indels 117; Gaps 3;
```

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Qy 1 GCCGAGCGCCGCGCAGTAGCGGTACTAAGTAGAGGCTGCTGGAGCGCCGCCACCCGGCAC 60
Db 35 GCCGAGCGCCAGTAGCCCGCGGGGCCCTGAGCAGAGCGCGTAGCTTGCAGCCGCCACCCGGCG 94
Qy 61 CAGCGGAGGCACAGATGCTTGGCAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 120
Db 95 CAGCGGAGGCACAAAGATGCGCGCTCTGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCT 154
Qy 121 CCGGTCTTTCCTTCCCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 155 ACAGCCTCGCCCTTCCC-----GCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 199
Qy 181 CCGGTGTCGCGCGCGCGCTCCCGCGCTCAGTCAGCCAGAACCTCGCTGCCCATCTCCGAGGCT 240
Db 200 CCGGTATCCGCGCGCGCTCCCGCGCTCGGTGCCAAGAACCTCGCTTCCCAATCTCTGAGGCT 259
Qy 241 GACTCTCTATCTCACCCCGGTTTGGACGCTCTCATACGTACAAATTAATCTGCTCTCTTGTG 300
Db 260 GACTCTCTATCTCACCCCGGTTTGGACGCTCTCATACGTACAAATTAATCTGCTCTCTTGTG 319
Qy 301 GATCTCTGCTCCACACACTTTAGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 360
Db 320 GATCTCTGCTCCACACACTTTATGTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 379
Qy 361 CCCTTCTCTGGGAAAGACCCCGAAGGATGACTGATGATGATGATGATGATGATGATGATGATG 420
Db 380 CCCTTCTCTGGGAGAGACCCCGAAGGATGACTGATGATGATGATGATGATGATGATGATGATG 439
Qy 421 AACTGAGGAAGAAAGCAAGAGGACGAATGTCAACAATTTTATCCAGATTTCTCGCC 480
Db 440 AACTGTAGGAAGAAAGCAAGAGAG- ----- 466
Qy 481 ATTGTCAATGCCCTCTACCTCTCCATCGTCGCGCACCTTCGCTTTTGTATCCGAAGTCGGG 540
Db 467 ----- 466
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Qy 541 GTTATTGATGTCCTCCAGTTTCCAGCAGGTTTGAAGACTTCAGAGCGCGCGCGCGGAAATGT 600
Db 467 -----GATGTGTCAGGTTTCCAGCAGGTTTGAAGACTTCAGAGTCGCGCGCGGAAATGT 520
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Qy	601	CCTTTTGAGCCAGCTCAACGGTCAGCAGCTGTAATAGCTGGGGCGTCTCTTACACCGCC	660
Db	521	CTTTTGGAGCGAGCTCAGCGGTCAGCAGCTGTAATAGCTGGGGGGTCTCTATGCTGCC	580
Qy	661	ACTGTGAAGRACITTCCTGGGACTGAGCCCATCATCTCCGAGCTGTGGTCTGAGCTGAG	720
Db	581	ACTGTGAAGAACACTACCTGGGAGCGAGCCAAATTATCACAGAGCAGTGGGTCTGCCGAG	640
Qy	721	GACTGGATTCGAACAGACACCTTGCTATCCTGGCTTAATGCTCCAGCCTTTGTGCGCAGCT	780
Db	641	GACTGGATTCGGACAGATACCTTGCCCTCTGGCTGAACGCCCGCAGCCTTTGTGCGCAGC	700
Qy	781	ATGTCCTGAGCCACGCTGAGTGGGGGATGAAGATGGAGACGATGAAATCTTTTTTTC	840
Db	701	GTGGCTTGAGCCACGCCGAATGGGGGATGAAGATGGAGACGAGAACTACTTCTTC	760
Qy	841	TTACGGAGACCTCCCGAGTGTGGACTCCTATGACGGCATCAAGTTCACAGAGTGCC	900
Db	761	TTTACGGAGACTTCCCGAGCATTTGACTCATACGAGCGCAATAAAGTCCACCGGTGCC	820
Qy	901	CGAGTGTGTGGGGGAGACCTTGGGGGCGAGGAAGACCCTTCAGCAGAGATGGACGACCTT	960
Db	821	CGTGTGTGGGGGAGACCTCGGGGCGGAGACCTCCAGCAGAGATGGACGACGCTT	880
Qy	961	CTAAGGCTGACCTGTGTGTGCCAGGCCCCAGAGATGCCGGGCTCCGGGTTCTGCAG	1020
Db	881	TTGAAGCTGACCTGTCTGTCCAGGGCCTGAGCATGGCGGGCTCCAGTGTCTTCAG	940
Qy	1021	GCTATGCGAGACTTCGGCCTCAGCCTGGAGCGGGAACCCCATCTTTTATGGGATCTTT	1080
Db	941	GATGTGTGTGTCTGACCTTGAGCTTGGGGCAGGGACTCCCATCTTTTATGGCATCTTT	1000
Qy	1081	TCCCTCCAGTGGGAAGAGCTGCCATCTCTGTCTGTGTGTGCTTCCGACCCCAAGACATC	1140
Db	1001	TCCTCCAGTGGGAGGGGCTACTATCTCTGTGTGTGTGCTTCCGACACACAGACATT	1060
Qy	1141	CGGCGAGTGTGAATGTGTCCCTTTAGAGAGCTAAACATGACTGCAACAGGGGACTGCCT	1200
Db	1061	CGGACAGTGTGAATGTGTCCCTTCAGAGAACTAAACATGACTGCAACAGGAGCTGCCT	1120
Qy	1201	GTCATGACACAGAGTGTGCCCGCCAGACCTGGAGAGTGCATCGCCACACACATCAAG	1260
Db	1121	GTCGTGACAAATGATGTGCCCGCCAGACCTGGAGAGTGCATCACCACAAACATGAAG	1180
Qy	1261	CTCCAGCAGTTTGGATCCTCACTCTCCTGCGACAGCGGTGCTCACCCTTATCAGAGAC	1320
Db	1181	CTCCGGCAGTTTGGCTCATCTCTCCTGCTGACCGGTACTCATCCTTCATCCGGGAC	1240
Qy	1321	CACCTCTCATGGAGCGCCGTGTCCCGGCTGACGGCGCCCGCTGCTGGTCACTACA	1380
Db	1241	CACCCACTCATGGACAGCCAGTGTTTCCAGCTGATGGCCACGCCCTGCTGGTCACTACA	1300
Qy	1381	GATACAGCCTATCTACAGTCTGTGGCCCCACAGGTTGACAGCCTCTCAGGGAAGAATAT	1440
Db	1301	GATACAGCCTATCTCAGAGTCTGTGGCCCCACAGGTTGACAGCCTCTCAGGGAAGAATAT	1360
Qy	1441	GACCTGCTTACCTGGGACAGAGATGACACCTCCACCGGCTGSCCATTTGGAGCT	1500
Db	1361	GATGTGCTTACCTGGGACAGAGATGGACCTCCACCGAGCAGTCCGAGTCCGGAGCT	1420
Qy	1501	CAGCTCAGTGTCTGGAGGATCTGGCCCTTGTCCAGAAACACAGCGGTTGAGAGCATG	1560
Db	1421	CAGCTCAGCGTCTTGAAGATCTGCGCCTTATCCAGAGCCACAGCCAGTTGAGAACATG	1480
Qy	1561	AAATTGTACACAGATTTGGTCTCTGGTGGGCTCCCATACTGAGTGCACAAAGTGAACACC	1620
Db	1481	AAATTGTACACAGCTGGCTCTGTTGGGCTCCCGTACTGAGTGCACAAAGTGAATACA	1540
Qy	1621	AGCAACTGTGCGCTCTCCAGAGCTGCTCGAGTGTATCCTGGCCCCAGGACCCGCTGTC	1680
Db	1541	ACCNACTGTGGCGCTCTCCAGAGCTGCTCAGAGTGATCTTGGCCCCAGGACCACTCTGT	1600
Qy	1681	GCCTGGAGCTTTCGGGCTTGATGTGTGTGGCCCCACGCCCGCGGAGACACCGCGGATGGTT	1740

Db	1601	GCCTGGAGCTTCGGGCTTGGATGAGTGTGTGGCCCATGCCGGGGAGCACCGAGGGTTGGTC	1660
Qy	1741	CAAGATATAGATCAGCGGATGCTCTCTTTTGTGTCCAAAGAACCTCGAGAACATCC	1800
Db	1661	CAGACATAGATCAGCAGATGTCCTCTTTTGTCTTAAGAGCCTCGAGAACGTCCA	1720
Qy	1801	GTAGTGTTTGAAGTTCCGGTGGCTACTGTGGGCCACGTGTCTGCCATTTCCCCCA	1860
Db	1721	GTAGTGTTCGAAGTTCCCGTGGCTACAGCTGCGCATGTGTCTTGCCATGTTCTCCA	1780
Qy	1861	TCGTGCTGGGCATCTCTGTGTGGCACACCGCCAGTGGAGTGTACTTGGCTCACTC	1920
Db	1781	TCAGCATGGGCATCTCTGTGTGGCACACCGCCAGTGGAGTGTACTTGGCTCACTC	1840
Qy	1921	AGGATGCACTAGAGGTGGTGGTACCCAGGGGCCATGGGGCTTATGCTTGGAGTGT	1980
Db	1841	CGGATGGACTGGAGGTGGTGGTACCCAGGGGCCATGGGGCTTATGCTTGGAA	1900
Qy	1981	CAGAGGGTGGAGCGCCCGCGTGGTGGCTTATAGCTTGGTGTGGGGCAGCCAGCGG	2040
Db	1901	CAGAGGGTGGGCAGCCCATGTGGTAGACGTTACAGCTTGGTATGGGCGCAGCCAG	1960
Qy	2041	GGACCTCAAAACGGGGCCACACGGTTGTGGGGCTGGATGGTGGCTTTCCTTGGGT	2100
Db	1961	GATGCTCCGAGCGGGGCCACAC---AGTGGGGCGGGACTGGCTGGCTTCTTCTTGGG	2017
Qy	2101	GTCTTTCAGCATCCCTCACTCTCCTCTGATTGGTGCCTCAGCAGCGTCGGCGACAG	2160
Db	2018	ATTCTCGCAGCATCCCTGACTCTCATCTGATTGGTCGGCTCAGCAGCGCGACAG	2077
Qy	2161	AGGAGGCTTCTAGCTAGAGACAAGTGGGCTTAGATCTGGGGGCTCCACCTTCTGGGAC	2220
Db	2078	AGGAACTTCTGGCTAGAGACAAGTGGGCTTGACCTGGGGCTCCACCTTCTGGGAC	2137
Qy	2221	ACAAGCTATAGTCAGGACCTCCTCTCTCTTCGCTTAAGATGAACGGCTGCCCTGGCC	2280
Db	2138	ACAAGCTTACAGCAAGACCTCCCTCCCTCTCTCTGAAGATGAGCGGTTGCCGCTGGCC	2197
Qy	2281	CTGGTAAGCGGGCAGTGGCTTTGGTGGCTTCCCTCCACCTTCCCTGCTGGATCTTGC	2340
Db	2198	CTGGCCAAGAGGGCAGTGGCTTTGGTGGATCTCACACCCCTTCTGCTTGGATCTTGC	2257
Qy	2341	CCAAGCCAGCCACATCCGGCTCACTGGGGCGGCTCTAGCCACGTGTGATGAGACCTCC	2400
Db	2258	CCAAGCCAGCCACATTCGGCTAAGTGGGCTCCTCTAGCCACATGTGATGAACATCC	2317
Qy	2401	ATCTAAAGCGGGGAAATGACTGCCAGCCATGAGCAGTCTCTGGAA	2448
Db	2318	ATCTAGAGCTGGGCAATGACCACTAGTGTATAAGTGATCACTGGAAC	2365
RESULT 6			
XX	AAx86127	ID	AAx86127 standard; DNA; 2894 BP.
XX	AC	AAx86127;	
XX	DT	15-SEP-1999	(first entry)
XX	DE	EST sequence for DNA encoding SBSEMN1.	
XX	KW	SBSEMN1: semaphorin; neurodegeneration; spinal injury; neuropathy;	
KW	KW	neuromuscular disorder; muscular dystrophy; psychiatric disorder;	
KW	KW	inflammatory disorder; developmental malformation; EST;	
KW	KW	expressed sequence tag; immune system disorder; cancer;	
XX	KW	viral infection; vaccine; ss.	
OS	XX	Homo sapiens.	
XX	PN	EP933425-A1.	
XX	PD	04-AUG-1999.	

[illegible]

Db 1481 AAATTGTACACAGCTGGCTCTGGTTGGCTCCCGTACTCCCGTACTGAGGTGACAAAGTAATACA 1540
Qy 1621 AGCAACTGTGGCGTCTCCAGAGCTGCTCGGAGTGTATCTCGGCCAGGACCCCGTGTGC 1680
Db 1541 ACCAAGTGTGGCGTCTCCAGAGCTGCTCAGAGTGTATCTCGGCCAGGACCCAGTCTGT 1600
Qy 1681 GCGTGGAGCTTCGGGCTTGAATGCTGTGTGGCCCGAGCCGCGGAGACCCGCGGATGTT 1740
Db 1601 GCGTGGAGCTTCGGGCTTGAATGCTGTGTGGCCCGATCCCGGGGAGCACCGAGGTGGTC 1660
Qy 1741 CAAGATATAGATCAGCGATGCTCTCTTTTGTGTCCTCAAAAGAACCTCGAGAACATCC 1800
Db 1661 CAAGACATAGATCAGCAGATGCTCTCTTTGTGTCCTAAAGAGCTCGAGAACATCCA 1720
Qy 1801 GTAGTGTAAAGTTCGGTGGCTACTGTGGCCAGCTGCTGTCATGTTTCCCCAGT 1860
Db 1721 GTAGTGTAAAGTTCGGTGGCTACAGCTGCGCATGTGCTTGCCATGTTTCCAAGC 1780
Qy 1861 TCTGCTGGCATCTGTGTGGCACCAGCCAGTGGAGTGAATGCTGCTACTCCCGG 1920
Db 1781 TCAGCATGGCATCTGTGTGGCACCAGCCAGTGGAGTGAATGCTGCTACTCCCGG 1840
Qy 1921 AGGATGGACTAGAGTGTGTGACCCAGCGGCGATGGGCGTATGCTTGCAGTGT 1980
Db 1841 CGGATGGACTAGAGTGTGTGACCCAGCGGCGATGGGCGTATGCTTGAATGT 1900
Qy 1981 CAGGAGGTGGAGCCCGCGTGTGTGCTTATAGCTTGTGGGCGAGCCAGCGG 2040
Db 1901 CAGGAGGTGGGCGAGCCCATGTGTAGCAGCTTACAGCTTGTATGGGCGAGCCAGA 1960
Qy 2041 GGACCTCAACCGGGCCACACCGTGTGGGCGTGGATGGTGGCTTCTCTGGGT 2100
Db 1961 GATGCTCCAGCGCGGCGCCACAC---AGTGGGCGGGAGTGGCTGGCTTCTTGGG 2017
Qy 2101 GTTCTGACGATCCCTCACTCTCTCTCTGATGCTGCCGTCAGCAGCGTGGGCGACAG 2160
Db 2018 ATTCTGCGCAGCATCCCTGACTCTCATCTGATGCTGGCGCTCAGCAGCGCGGACAG 2077
Qy 2161 AGGAGCTTCTAGTAGACAAAGGTGGGCTTATAGTCTGGGCGCTCCACCTTCTGGGACC 2220
Db 2078 AGGAACTTCTGGCTAGACAAAGGTGGGCGTGGACCTGGGCGCTCCACCTTCTGGGACC 2137
Qy 2221 ACAAGCTATGTCAGACCCCTCCCTCTCTGCTGCTGAAGATGAACGGTGGCCCTGGCC 2280
Db 2138 ACAAGCTACAGCAAGACCCCTCCCTCCCTCTCTGAGATGAGCGGTGGCGCTGGCC 2197
Qy 2281 CTGGGTAAAGCGGGCAGTGGTGTGGCTTCCCTCCACCGTCTCTGCTGATGTTTGC 2340
Db 2198 CTGGCCAGAGGGGCGAGTGGCTTGTGGATTTCTCACCACCCCTTCTGCTGATCTTGC 2257
Qy 2341 CCAAGCCAGCCACATCCGCTCACTGGGCGCTCTAGCCACGCTGTGATGAGACCTCC 2400
Db 2258 CCAAGCCAGCCACATCCGCTCACTGGGCTCTCTAGCCACATGTGATGAACATCC 2317
Qy 2401 ATCTAAAGCGGGGAAATGACTGCCAGCCATGACAGTCTCTGGAAC 2448
Db 2318 ATCTAGAGCTGGGCAAAATGACCACCTAGTGTATAAGTGTGATGATCTGGAAC 2365

RESULT 7
AAV07281
ID AAV07281 standard; cDNA to mRNA; 2315 BP.
XX
AC AAV07281;
XX
DT 08-SEP-1998 (first entry)
XX
DE Human semaphorin W encoding cDNA with 3'UTR.
XX
KW Human; semaphorin W; nerve extension inhibitor; antiallergic; anticancer;
KW immunosuppressant; gene therapy; diagnosis; research reagent; ds.
XX
OS Homo sapiens.

XX
FH Location/Qualifiers
CDS 1..1764
FT /*tag= a
FT /*product= "semaphorin W"
FT 1765..2315
FT /*tag= b
XX
PN W09815628-A1.
XX
PD 16-APR-1998.
XX
PF 03-OCT-1997; 97WO-JP03549.
XX
PR 09-OCT-1996; 96JP-0287636.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
XX
PI Kikuchi K, Kimura T;
XX
XX WPI: 1998-261015/23.
DR P-PSDB; AAW51314.
XX
PT Nerve extension inhibitor protein semaphorin W - is useful as
PT therapeutic drug and diagnostic and research reagent
XX
PS Claim 2; Page 65-66; 90pp; Japanese.
XX
CC The present sequence encodes human semaphorin W. Semaphorin W and
CC its derivatives are nerve extension inhibitors which are useful as
CC antiallergic, immunosuppressant and anticancer agents. The DNA
CC encoding semaphorin W can also be used in gene therapy, e.g. using
CC a viral vector. The proteins, peptides, DNA and antibodies which
CC recognise the protein or peptides, can be used as diagnostic or
CC research reagents. Semaphorin W can be used as a screen for
CC semaphorin W antagonists with possible therapeutic use.
XX
SQ Sequence 2315 BP; 463 A; 640 C; 670 G; 542 T; 0 other;

Query Match 35.0%; Score 1404.2; DB 19; Length 2315;
Best Local Similarity 86.4%; Pred. No. 2.5e-314; Indels 3; Gaps 1;
Matches 1563; Conservative 0; Mismatches 243;
Qy 640 GGGGGCGCTCTACACCGCCACTGTGAAGAACTTCTCGGGAGCTGAGCCCATCATCTCC 699
Db 1 GGGGGTGTCTCTATGCTGCCACTGTGAAAACTACCTGGGACGAGCAATTTATCAC 60
Qy 700 CGAGCTGTGGTTCGAGCTGAGGACTGGATTTCGAACAGAGACCTTGTCTATCTCGCTTAT 759
Db 61 AGAGCAGTGGGTGCTGCCGAGGACTGGATTTCGACAGATACCTTCCCTTGGCTGAAC 120
Qy 760 GCTCCAGCCTTTGTGCGAGCTATGCTGCTGAGCCCGAGCTGAGTGGGGGATGAAGATGA 819
Db 121 GCGCCAGCCTTTGTGCGAGCGTGGCTTGAAGCCAGCGCAATGGGGGATGAAGATGA 180
Qy 820 GACGATGAATCTTTTTTTTCTTACGAGAGACCTCCCGAGTGTGGAGCTCTATGAGCGC 879
Db 181 GACGACGAATCTACTTCTTTTACGAGAGCTTCCCGAGCATTTTACTCATACGAGCGC 240
Qy 880 ATCAAGGTCCCAAGAGTGGCCGAGTGTGCGGGGGACCTTGGGGGAGGAGACCCCTT 939
Db 241 ATTAAGTCCCAAGGTGGCCGAGTGTGCGGGGGACCTTGGGGGAGGAGACCCCTC 300
Qy 940 CAGCAGATGAGCAGCCTTTCTGAAGCTGACCTGCTGTGCCCGAGCGCCCGAGCATGCG 999
Db 301 CAGCAGATGAGCAGCCTTTTGAAGCTGACCTGCTGTGCCAGAGCGCTGAGCATGCG 360
Qy 1000 CGGGCTCCGGGGTTCGAGGCTATGCGAGAGTTCGCGCTCAGCTCTGAGCGCGGAAC 1059
Db 361 CGGGCTCCAGTGTCTCGAGGATGTTGCTGTGCTTCGACCTGAGCTTTGGGCGAGGACT 420
Qy 1060 CCCATCTTTTATGGGATCTTTTCTCCAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1119

Db 421 CCCATCTTTATGCACTCTTTTCTTCCAGTGGGAGGGGCTACTATCTCTGCTGTCTGT 480
Qy 1120 GCCTTCGACCCCAAGACATCCGGGCACTGCTGAATGGTCCCTTTAGAGAGCTAAACAT 1179
Db 481 GCCTTCGACCAACAGACATTCGGACAGTCTGATGATGGTCCCTTCAGAGAACTAAACAT 540
Qy 1180 GACTGCAACAGGGGATGCCTGTCTCATGGACAAGAGGTGCCCCAGCCAGACCTTGGAGAG 1239
Db 541 GACTGCAACAGAGACTGCGCTGTCTGTGGACAAATGATGTGCCCCAGCCAGACCTTGGAGAG 600
Qy 1240 TGCATGCCACACACATGAAGCTCCAGACAGTTTGGATCCTCACTCTCCCTGCCAGACGC 1299
Db 601 TGCATCCACACACATGAAGCTCCGGCCTATGGCTCACTCTCTCCCTGCCAGACGC 660
Qy 1300 GTGCTCACTTTATCAGAGACCAACCTCTCATGACAGAGCGGTGTTCCCGGCTGACGGC 1359
Db 661 GTACTCACTTATCCGGGACCACTCATGACAGGCGAGTGTTCACAGCTGATGGC 720
Qy 1360 CGCCCTCTGCTGCTACTACAGATACAGCTATCTCAGAGTCGTGGCCACAGAGGTGACC 1419
Db 721 CACCCCTGCTGCTACTACAGATACAGCTATCTCAGAGTCGTGGCCACAGAGGTGACC 780
Qy 1420 AGCCTCTCAGGAAGAATATGACGTCTCTACCTGGGACAGAGATGGACACTCCAC 1479
Db 781 AGCCTCTCAGGAAGAATATGATGTCTCTACCTGGGACAGAGATGGACACTCCAC 840
Qy 1480 CGGCTGTGGCATTTGGAGCTCAGCTCAGTGTCTTGGAGGATCTGGCCTTGTCCAGAA 1539
Db 841 CGACGACTGGGATCGGAGCTCAGCTCAGCTCAGGCTTCTGAAGATCTGGCTTATCCAGAG 900
Qy 1540 CCACAGCGGTTGAGACATGAATTTACACAGATTGGCTTCCTGGTGGCTCCCTACT 1599
Db 901 CCACAGCGGTTGAGACATGAATTTACACAGCTGGCTTCCTGGTGGCTCCCTACT 960
Qy 1600 GAGGTGACACAGTGAACACCACTGTGGCGTCTCCAGAGCTGCTCGGAGTGTATC 1659
Db 961 GAGGTGACACAGTGAATGAACCACTGTGGCGTCTCCAGAGCTGCTCAGAGTGCATC 1020
Qy 1660 CTGGCCAGGACCCGCTGTGGCGCTGGAGCTTCGGGCTGATGCTGTGGCCACAGCC 1719
Db 1021 CTGGCCAGGACCCAGTCTGTGGCTGGAGCTTCGGGCTGGATGATGTGTGGCCCATGCC 1080
Qy 1720 GGCAGCACCGCGGGATGGTTCAAGATATAGATCAGCGGATGTCTTCTTTGTGTCCA 1779
Db 1081 GGGGAGCACCGGAGGTGGTCCAAAGACATAGATCAGCAGATGTCTCTCTTTGTGCTCT 1140
Qy 1780 AAAGAACCTGGAGAACATCCGTAGTCTTGAAGTTCGGTGGCTACTGTGGGCCACAGTG 1839
Db 1141 AAAGAGCTGGAGAACGTCAGTAGTGTGTTGAAGTTCGGTGGCTACTAGCTGGCGCATGTG 1200
Qy 1840 GTCTTGCCATGTTCCCGCAGTCTGCTGGGCACTCTGTGTGGCACCAAGCCAGTGA 1899
Db 1201 GTCTTGCCATGTTCTCCAACTCAGCATGGCATCTGTGTGGCACCAAGCCAGTGA 1260
Qy 1900 GTGACTGGCTTACTCCCGGAGGGATGGACTAGAGTGTGTGTGACCCAGGCGGCATG 1959
Db 1261 GTGACTGCACTCAACCCCGCGGATGGACTGGAGTGTGTGTGACCCAGGCGGCATG 1320
Qy 1960 GGGGCTTATGCTTCGAGTGTCAAGAGGTGGAGCCCGCCGCTGGTGGCTTATAGC 2019
Db 1321 GGGCTTATGCTGTGAATGTCAAGAGGGTGGGACAGCCCATGTGGTGAAGCTTACAGC 1380
Qy 2020 TTGCTGTGGGACAGCCAGCGGGGACCTCAAAACCGGGCCACACCGTGTGGGGCTTGA 2079
Db 1381 TTGATTTGGGACAGCCAGGAGATGCTCCGAGCCGGGCCACAC- ---AGTGGGGCGGGA 1437
Qy 2080 TTGGTGGCTTCTCTCGGTGTTCTTCAGACATCCCTCACTCTCTCTCTGATTTGTCGC 2139
Db 1438 CTGGCTGGCTTCTCTTTGGGATCTCGCAGCATCCCTGACTCTCATCTGATTTGTCGC 1497
Qy 2140 CGTCAGCAGCTCGGCGACAGAGGAGCTTCTAGCTAGACAAAGGTGGGCTTATAGTCTG 2199
Db 1498 CGTCAGCAGCGACGCGACAGAGGAACTTCTGGCTAGAGACAAAGGTGGGCTTGGACCTG 1557

Qy 2200 GGGCTCCACCTTCTGGGACCAAGCTATAGTCAGGACCTCCCTCTCTCTTCCCTCGAA 2259
Db 1558 GGGCTCCACCTTCTGGGACCAAGCTACAGCCAAAGACCTCCCTCCCTCTCTCGAA 1617
Qy 2260 GATGAACGGCTGCCCCCTGGGCTGGTAAGGGGGCAGTGGTTTTGTGTGGCTTCCCTCCA 2319
Db 1618 GATGAGCGGTGGCGCTGGCCCTGCCAAGAGGGGAGTGGCTTTGTGGATTCTCACCA 1677
Qy 2320 CCCTTCTCTGGATTCTTGCCCAAGCCAGCCACATCCGGCTCACTGGGCGCCTCTA 2379
Db 1678 CCCTTCTCTGTATCTTGCCCAAGCCAGCCACATCCGGCTCACTGGGCTTCTCTA 1737
Qy 2380 GCCACGTGTGATGAGACCTCCATCTAAAGCGGGGAAATGATGCCAGGCATGAGCAGT 2439
Db 1738 GCCACATGTGATGAACATCCATCTAGAGCTGGGCAATGACCACTAGTGATTAAGTGAT 1797
Qy 2440 CTCTGGAAC 2448
Db 1798 CACTGGAAC 1806

RESULT 8

AAV07282 .
ID AAV07282 standard; cDNA to mRNA; 1761 BP.
XX
AC AAV07282;
XX
DT 08-SEP-1998 (first entry)
XX
DE Human semaphorin W encoding cDNA.
XX
KW Human; semaphorin W; nerve extension inhibitor; antiallergic; anticancer; immunosuppressant; gene therapy; diagnosis; research reagent; ds.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1764
FT /tag= a
FT /product= "semaphorin W"
XX
PN WO9815628-A1.
XX
PD 16-APR-1998.
XX
PF 03-OCT-1997; 97WO-JP03549.
XX
PR 09-OCT-1996; 96JP-0287636.
XX
PS (SUMO) SUMITOMO PHARM CO LTD.
XX
PA Kikuchi K, Kimura T;
XX
PI
XX
DR WPI; 1998-261015/23.
XX
DR P-PSDB; AAW51314.
XX
PT Nerve extension inhibitor protein semaphorin W - is useful as
PT therapeutic drug and diagnostic and research reagent
XX
PS Claim 2; Page 67-68; 90pp; Japanese.
XX
CC The present sequence encodes human semaphorin W. Semaphorin W and
CC its derivatives are nerve extension inhibitors which are useful as
CC antiallergic, immunosuppressant and anticancer agents. The DNA
CC encoding semaphorin W can also be used in gene therapy, e.g. using
CC a viral vector. The proteins, peptides, DNA and antibodies which
CC recognise the protein or peptides, can be used as diagnostic or
CC research reagents. Semaphorin W can be used as a screen for
CC semaphorin W antagonists with possible therapeutic use.
XX
SQ Sequence 1761 BP; 349 A; 511 C; 521 G; 380 T; 0 other;

CC substitutions in the amino acids. The NOVX polypeptides are useful in
CC manufacturing a medicament for treating a syndrome associated with a
CC human disease, which is a pathology associated with the NOVX polypeptide.
CC The NOVX polypeptides, nucleic acids and antibodies are useful for
CC diagnosing, preventing or treating diseases such as atherosclerosis,
CC hypertension, cancer, tuberculous sclerosis, Alzheimer's disease,
CC Parkinson's disease, multiple sclerosis, cachexia, anorexia, obesity,
CC infertility, atherosclerosis, hypertension, scleroderma, haemophilia,
CC dyslipidaemias, diabetes, autoimmune disease, immunodeficiencies, AIDS,
CC or graft-versus-host disease. The nucleic acids are useful as
CC hybridisation probes, in chromosome mapping, tissue typing, preventive
CC medicine, or pharmacogenomics. This polynucleotide sequence represents
CC the coding DNA of a NOVX protein of the invention.

XX
SQ Sequence 777 BP; 153 A; 230 C; 208 G; 186 T; 0 other;

Query Match 13.2%; Score 527.4; DB 25; Length 777;
Best Local Similarity 90.2%; Pred. No. 6.8e-112;
Matches 564; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
Qy 193 CGCGTCCCGCGCTCAGTGCAGGAGCCGCTGCGCCATCTCCGAGGCTGACTCTATCTC 252
Db 7 CGCGTCCCGCGCTCAGTGCAGGAGCCGCTGCGCCATCTCCGAGGCTGACTCTATCTC 66
Qy 253 ACCCGGTTGAGCGTCTCATACGTACAACTGCTGCTCTCTGCTGCTGCTGCTGCTGCT 312
Db 67 ACCCGGTTGAGCGTCTCATACGTACAACTGCTGCTCTCTGCTGCTGCTGCTGCTGCT 126
Qy 313 CACACACTTACGTCGCTGCGGACGAGTACGATCTTCAACCTCCCTCTCTGCG 372
Db 127 CACACACTTATGTTGGCGCCCGGACACCATCTTCGCTTATCCCTGCGCTTCTCAGG 186
Qy 373 GAAAGACCCCGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
Db 187 GAGAGACCCCGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 246
Qy 433 AAAGCGAAGAAAGAGGAGGAGTGCACAACTTTATCCAGATCTTCGCCATTTGCAATGCC 492
Db 247 AAAGCGAAGAAAGAGGAGGAGTGCACAACTTTTCCAGATCTTCGCCATTTGCAATGCC 306
Qy 493 TCTCACCTCTCTCAGTGGCGGACCTCTGCTTTTATCCGAGTGGCGGCTGCTGCTGCTGCT 552
Db 307 TCTCACCTCTCTCAGTGGCGGACCTCTGCTTTTATCCGAGTGGCGGCTGCTGCTGCTGCT 366
Qy 553 TCCAGTTTCCAGCAGGTTGAAAGACTTGAGAGCGCGCGGGGAAATGCTCTTTTGGCCCA 612
Db 367 TCCAGTTTCCAGCAGGTTGAAAGACTTGAGAGTGGCGGGGAAATGCTCTTTTGGCCCA 426
Qy 613 GCTCAACGGTCAGCAGCTGTAATGGCTGGGGGCTCTCTACACCGGCTGCTGCTGCTGCT 672
Db 427 GCTCAGGGTTCAGCAGCTGTAATGGCTGGGGGCTCTCTATGCTGCTGCTGCTGCTGCT 486
Qy 673 TTCCTGGGAGTGAAGCCATCATCTCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
Db 487 TACCTGGGAGCGGAGCAATATATCAGCAGACAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 546
Qy 733 ACAGAGACCTTGTCTGCTTAAATGCTCCAGCCTTTTGTGCGAGCTATGCTGCTGCTGCT 792
Db 547 ACAGATACCTTGTCTGCTTAAATGCTCCAGCCTTTTGTGCGAGCTATGCTGCTGCTGCT 606
Qy 793 CCAGCTGAGTGGGGGATGAAGATG 817
Db 607 CCAGCCGAATGGGGGATGAAGATG 631

RESULT 12

ID ABL89791

XX ABL89791 standard; cDNA; 671 BP.

AC ABL89791;

XX ABL89791;

DT 24-MAY-2002 (first entry)

XX

DE Human polynucleotide SEQ ID NO 353.
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; antitumor;
KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein; gene; ss.
OS Homo sapiens.
XX WO200190304-A2.
PN 29-NOV-2001.
PD 18-MAY-2001; 2001WO-US16450.
PF 19-MAY-2000; 2000US-205515P.
PR (HUMA-) HUMAN GENOME SCI INC.
XX Birse CE, Rosen CA;
PI WPI; 2002-122018/16.
DR P-PSDB; ABB89382.
XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive,
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders -
XX
PS Claim 4; SEQ ID NO 353; 2081pp + Sequence Listing; English.
XX The invention relates to novel genes (ABL89449-ABL90853) and proteins
CC (ABB9040-ABB90444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 671 BP; 134 A; 176 C; 214 G; 140 T; 7 other;

Query Match 12.6%; Score 505.2; DB 24; Length 671;
Best Local Similarity 86.6%; Pred. No. 8.8e-107;
Matches 582; Conservative 7; Mismatches 10; Indels 3; Gaps 3;
Qy 1387 GCCTATCTCAGAGTCGTGGCCACAGGCTGACAGCTCTCAGGAGAAATATGACGTG 1446
Db 1 GCCTATCTCAGAGTCGTGGCCACCA-GGTGACAGCTCTCAGGAGAAATATGATGTG 59
Qy 1447 CTCTACCTGGGGACA-GAGGATGGACACCTCCACCGGCTGTGGCATTTGAGCTCAGCT 1505
Db 60 CTCTACCTGGGGACATGAGGATGGACACCTCCACCGAGCTGCGGAGCTCAGCT 119
Qy 1506 CAGTGTCTTGGAGATCTGGCTTTGTTCCAGACACACAGCCGGTTGAGACATGAATTT 1565
Db 120 CAGCGTCTTGAAGATCTGGCTTTATTTCCAG-AGCAGCAGCTGTTGAGAACATGAATTT 178
Qy 1566 GTACACGATTTGGCTCTCTGGTGGCTCCCTACTGAGGTGACACAAAGTGAACACGAA 1625
Db 179 GTACACAGCTGGCTCTCTGGTGGCTCCCTACTGAGGTGACACAAAGTGAACACCA 238

Db 956 ATATGGGGGGGACGACCCCTGCGAGAGGAAGTGGACCAAGTTCCTGAAGCGCGGGCTGG 1015
Qy 977 TGTGCCCAGGCGCCGAGCATGGCGGGCTCCGGGGTTCTGCAGGCTATGCGAGAGCTTC 1036
Db 1016 CATGCTCTGCCCGAAGTGGCAGCTTACTTCAACAGCTGCAGGGGATG---CACACCC 1072
Qy 1037 GGCCCTCAGCTGAGCGGGAAACCCCACTTTTATGGGATCTTTTCTCCAGTGGGAAG 1096
Db 1073 TGCAGGACACCTCTGCGCACAACACCACTTCTTTGGGTTTTCAGAGCACAGTGGGGTG 1132
Qy 1097 GAGTGCATCTCTGCTGTGCTGCTCCGACCCCAAGACATCCGGGCAGTCTGAATG 1156
Db 1133 ACATGTACCTGTGGGCATCTGTAGTACCAGTTGGAAGAGATCCAGCGGGTGTGAGG 1192
Qy 1157 GTCCCTTAGAGAGCTAAACATGACTGCAACAGGGGACTGCTGTCTATGGACAACGAGG 1216
Db 1193 GCCCTATAGAGTACCATGAGGAAGCCAGAGTGGGACCGCTACACTGACCT---G 1249
Qy 1217 TGCCCCAGCCAGACCTGGAGAGTGATCGCCCAACACATGAAGCTCCAGCAGTTGGAT 1276
Db 1250 TACCCAGCCCTCGCCCTGGCTGCTGCTGCTAATAACAACCTGGCATCGCGCCAGCGGTACACCA 1309
Qy 1277 CCTCAGCTCTCCCTGCCAGACCGGCTGCTACCTTTATCAGAGACCACTCTCATGGACA 1336
Db 1310 GCTCCCTGGAGCTACCCGACAACATCTCACTTCTGTCGAAGAGCACCCGCTGATGGAGG 1369
Qy 1337 GGCCCGTGTCCCGGCTGACGGCGCCGCCCTGCTGCTCACTACAGATACAGCCTATCTCA 1396
Db 1370 AGCAGTGGGGCTCGGTGGAGCGCCCTGCTGCTGAAGAGGGCACCACTTCACCC 1429
Qy 1397 GAGTGTGGCCACAGGTTGACAGCCTCTCAGGGAAAGATATGAGCTGCTCTACCTGG 1456
Db 1430 ACCTGTGGCCGACCGGGTTACAGGACTTGATGGAGCCACTATACAGTGTGTTTCATTG 1489
Qy 1457 GGACAGAGATGGACACCTCCAGCGGCTGTCGCAATTGGAGCTCAGTCTAGTCTTTGG 1516
Db 1490 GCRAGAGAGCGGTGCTGCTCAAGCTGTGAGCCTGGGGCCCTGGGTTACCTGATTG 1549
Qy 1517 AGGATCTGGCCTTGT---CCCAAGAACACAGCGGTTGAGAGCATGAAATTTGACCAAG 1573
Db 1550 AGGAGCTGCAGCTGTTTGACAGGAGCCCATGAGAAGCTTGGTCTATCTCAGAGCAAGA 1609
Qy 1574 ATTGGCTCCTGGTGGGCTCCCACTAGAGTGACACAAGTGAACACAGCAACTGTGGCC 1633
Db 1610 AGCTGCTCTTTGGCGGCTCCGCTCTCAGCTGGTGCAGCTGCCCGTGGCGGACTGCATAA 1669
Qy 1634 GTCTCCAGAGCTGCTCGGAGTGTATCTGCGCCAGGACCCGCTGTGCGCCTGGAGCTTCC 1693
Db 1670 AGTATCGCTCTGTGCAAGTGTGCTCGCCGGGACCCCTATTGCGCCTGGAGCGTCA 1729
Qy 1694 GGCTTGATGTTGTGGCCACGCGCGGA 1724
Db 1730 ACACAGCCGCTGTGTGGCGTGGTGGCCA 1760

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Job time : 991.19 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 25, 2003, 19:14:04 ; Search time 14345.7 Seconds
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Title: US-09-284-180a-1

Perfect score: 4008

Sequence: 1 gccgagggccgcgcagtagc.....aaaaaaaaaaaaaaaaaaaa 4008

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

1: gb_ba:*
2: gb_hgt:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
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29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
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40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4008	100.0	4008	10	AB002563	AB002563 Rattus no
2	3109.2	77.6	4002	10	AB021291	AB021291 Mus muscu
3	2173	54.2	25079	2	AC135520	AC135520 Rattus no
4	2077.2	51.8	2354	10	AF038652	AF038652 Mus muscu
5	1954	48.8	4293	9	HS0801526	AL136552 Homo sapi
6	1875.2	46.8	2971	6	AX136143	AX136143 Sequence
7	1875.2	46.8	2971	6	BD123524	BD123524 Secretary
8	1875.2	46.8	2971	9	AK075384	AK075384 Homo sapi
9	1867.8	46.6	2948	9	BC038411	BC038411 Homo sapi
10	1673.6	41.8	2893	6	AX003081	AX003081 Sequence
11	1673.6	41.8	2893	6	BD177663	BD177663 SBSENN1 p
12	1673.6	41.8	2893	6	E35443	E35443 SBSENN1 p
13	1673.6	41.8	2894	6	AX003083	AX003083 Sequence
14	1673.6	41.8	2894	6	BD177664	BD177664 SBSENN1 p
15	1673.6	41.8	2894	6	E35444	E35444 SBSENN1 p
16	1483.8	37.0	3205	10	AB022311S6	AB022311 Mus muscu
17	1483.8	37.0	162691	10	AC003061	AC003061 Mouse Chr
18	1483.8	37.0	214837	10	AC007305	AC007305 Mus muscu
19	1475.8	36.8	109332	2	AC134899	AC134899 Mus muscu
20	1464	36.5	2672	9	AB021292	AB021292 Homo sapi
21	1201.4	30.0	2507	9	BC018361	BC018361 Homo sapi
22	1199.8	29.9	2400	9	AB022317	AB022317 Homo sapi
23	1034	25.8	1913	9	AF053369	AF053369 Homo sapi
24	692.8	17.3	2669	9	AB047604	AB047604 Macaca fa
25	654	16.3	799	6	AX003085	AX003085 Sequence
26	654	16.3	799	6	BD177665	BD177665 SBSENN1 p
27	654	16.3	799	6	E35445	E35445 SBSENN1 p
28	539	13.4	110000	2	AL451003_2	Continuation (3 of
29	539	13.4	126228	9	AC006543	AC006543 Homo sapi
30	539	13.4	234523	9	AC006544	AC006544 Homo sapi
31	527	13.1	163903	9	AC007387	AC007387 Homo sapi
32	477.2	11.9	64154	2	AL451003_3	Continuation (4 of
33	408	10.2	669	6	AX136484	AX136484 Sequence
34	408	10.2	669	6	BD123724	BD123724 Secretary
35	373.6	9.3	3293	6	AX174731	AX174731 Sequence
36	251.8	6.2	2155	6	AX060303	AX060303 Sequence
37	248.6	6.2	2156	6	AX060313	AX060313 Sequence
38	248.6	6.2	2284	6	AX060305	AX060305 Sequence
39	248.6	6.2	2284	6	AX060305	AX060305 Sequence
40	248.6	6.2	2646	6	AX704763	AX704763 Sequence
41	248.6	6.2	3776	6	BD171174	BD171174 Novel gen
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44	247.8	6.2	3112	6	AX528279	AX528279 Sequence
45	247	6.2	3781	6	AX376386	AX376386 Sequence

ALIGNMENTS

RESULT 1
AB002563
LOCUS
DEFINITION
Rattus norvegicus mRNA for semaphorin W, complete cds.
ACCESSION
AB002563
VERSION
AB002563.1 GI:4519426
KEYWORDS
semaphorin W.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (sites)
AUTHORS
Encinas,J.A., Kikuchi,K., Chedotal,A., de Castro,F., Goodman,C.S.
and Kimura,T.

TITLE	Cloning, expression, and genetic mapping of Sema W, a member of the semaphorin family
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (5), 2491-2496 (1999)
MEDLINE	99162633
PUBMED	10051670
REFERENCE	2 (bases 1 to 4008)
AUTHORS	Kimura, T. and Kikuchi, K.
TITLE	Direct Submission
JOURNAL	Submitted (31-MAR-1997) Toru Kimura, Sumitomo Pharmaceuticals Research Center, Discovery Research Laboratories II; 1-98, Kasugade Naka 3-chome, Konohana-ku, Osaka, Osaka 554, Japan (E-mail: tkimura@sumitomopharm.co.jp, Tel:06-466-5228, Fax:06-466-5491)

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NMKLQFGSSLSLPQRLVLTIRDHPLMDRPVPADGQRLPVTDTAYLRVAHRVTSLT
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CPKEGEPHVPFEVQVATVGHVTVLSPSSASWASCVWHPQSGVTALTPRDGLGVVLT
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     775 a  1135 c  1141 g   957 t

BASE COUNT
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ORIGIN

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Best Local Similarity	100.0%;	Pred. No. 0;		
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Db	1			
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QY	61	CAGGCGGAGCCAGAGATGTTGCCAGGGCCGAGCGCCCCCGCGGGCCCCCGCGCGCCT	120	
Db	61			
		1 CAGGCGGAGCCAGAGATGTTGCCAGGGCCGAGCGCCCCCGCGGGCCCCCGCGCGCCT	120	
QY	121	CGGGTCTTTCCCTTCCCGCGCGGCTGTGCGTGCTGCTGCTGCTGGCGATATAAGCGCC	180	
Db	121			
		1 CGGGTCTTTCCCTTCCCGCGCGGCTGTGCGTGCTGCTGCTGCTGGCGATATAAGCGCC	180	
QY	181	CGGGTCTGGCGGCGTCCCGCGCTCAGTGCCACAGAACCTCGCTGCCCATCTCCGAGGCT	240	
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		1 CGGGTCTGGCGGCGTCCCGCGCTCAGTGCCACAGAACCTCGCTGCCCATCTCCGAGGCT	240	
QY	241	GACTCTATCTCACCGGTTTGACGGTCTCATACGTACAATTACTCTGCTCTCTCTTG	300	
Db	241			
		1 GACTCTATCTCACCGGTTTGACGGTCTCATACGTACAATTACTCTGCTCTCTCTTG	300	
QY	301	GATCCTGCCTCCACACACTTTACGTCGGTGACGGGATAGCATCTTCGCTTTAACCCCTC	360	
Db	301			
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QY	361	CCCTTCTCTGGGAAAGACCCCGAAGGATCGACTGGATGGTACCTGAGACTCAGACAG	420	

[illegible]

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Db	3236	TTGAGGGATGACAAAAG- ----GAACCCAGAAAAGTGTAGAAAATTTACAAGCAGATT	3289
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Db	3290	CAAGAAATTTGCTCTCAGTGACTTTACCCTTGCCCTAAAGCAGGAGTCCCTTAGC- ----	3345
Qy	3298	GTCGTGTGACTCCCTGAAATTTGATGCGTGTGTGACTCCCTGAAATTTGATGCAAGTG	3357
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Qy	3358	TCGTG	3417
Db	3398	TGCGTGGTG	3433
Qy	3418	CATGTGTGTTTGATGGCTTTTCATCAGATTCTCAAGGCCTTAAAGCAGTTTAAAGCACCAG	3477
Db	3434	-----TGATGGCTTTTCATCAGATTCTCAAGGCCTTAAAGCAGTTTAAAGCACCAG	3483
Qy	3478	GCCTATAGTCACACACTTGGGCCACATGGAGGAGTGTGCT-CTCTGAGGAGTTTCCT	3536
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Qy	3537	CCCTGGC- --CTGCCTCAGGCCAGCCCTGGACACATGCTGCTGGAGACCCACATCTC	3593
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Db	3604	TCCAGTCCCTCCGGAAGCTAGTGAAGCTAGGCTCTGACGTGCTTGAAGCACCATCCG	3663
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Db	3784	TTCCAGTTGAAGTTTCTGTTCTACTTTCCCTTGACAGCAGCTGTGTAATTTACTCAAGATC	3843
Qy	3821	CCCTT-CGTTTGAGTTCCCGGTGGCTTTGAGTAGGATCTTTGGCGTGGCATCTAACCTA	3879
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Qy	3880	GCAGCATTTGATCGTTTCAT-TGTAAAGTGGGATATACCTACCTCAGGTTTGTGTCAAGGA	3938
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RESULT 3

AC135520/C

LOC

DEFINITION *Rattus norvegicus* clone CH230-182B14, WORKING DRAFT SEQUENCE, 10

250709 bp DNA Linear

250709 bp DNA linear HTG 15-NOV-2002

AC135520

Rattus norvegicus clone CH230-182B14, WORKING DRAFT SEQUENCE, 10

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL
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2					
3					
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REFERENCE
AUTHORS
TITLE
JOURNAL

unordered pieces.

AC135520
AC135520.2 GI:25007227
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 250709)
Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
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Fraser,C.G., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Georgellis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
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Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokelemeh,O., Okwuonu,G., Olarunpsagoon,A., Pal,S., Parks,K.,
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Puzao,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
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Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willison,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Niederstock,C. and Gibbs,R.A.

[illegible]

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Db	198037	ACGTATAAATAAGCATTACCCACAGCAGTAGA	198005
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DEFINITION		Mus musculus semaphorin M mRNA, partial cds.	
ACCESSION		AF038652	
VERSION		AF038652.1	GI:4104674
KEYWORDS			
SOURCE		Mus musculus (house mouse)	
ORGANISM		Mus musculus	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
TITLE		Jang, W., Spilson, S.V., Hua, A., Roe, B. and Meisler, M.H.	
JOURNAL		Large-scale comparative sequence analysis of human and mouse	
REFERENCE		genomic DNA reveals coding regions of three new genes	
AUTHORS		Unpublished	
TITLE		2 (bases 1 to 2354)	
JOURNAL		Jang, W., Spilson, S.V. and Meisler, M.H.	
FEATURES		Direct Submission	
source		Submitted (12-DEC-1997) Human Genetics, University of Michigan,	
		4708 MS II, Box 0618, Ann Arbor, MI 48109-0618, USA	
		Location/Qualifiers	
		1..2354	

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Db	2280 CTTGTGATCACACGCTCAGTGTCTCTCTCGACCTGGACCTGGA 2319		
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DEFINITION	Homo sapiens mRNA; cDNA DKFZp761O15121 (from clone DKFz761O15121); complete cds.		
VERSION	AL136552		
KEYWORDS	All36552.1 GI:13276610		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 4293)		
AUTHORS	Poustka,A., Klein,M., Mewes,H.W., Gassenhuber,J. and Wiemann,S.		
TITLE	Direct Submission		
JOURNAL	Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY		
COMMENT	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ). Email s.wiemann@dkfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp761O15121) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.		
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ORIGIN			
Query Match	48.8%; Score 1954; DB 9; Length 4293;		
Best Local Similarity	72.3%; Pred. No. 0;		

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Qy 481 ATTGTCAATGCCCTCCTACCTCCTCACGTGGGGACCTTCGCTTTTGTATCCGAAGTCGGG 540
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Qy 841 TTACAGGAGACTCCCGAGTGTGGACTCTATGAGCGCATCAAGCTCCCAAGAGTGGCC 900
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Qy 961 CTGAAGCTGACCTGCTGTGCCAGGCGCCGAGCATGCGGGCTCCGGGGTCTCGAG 1020
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Db 1333 CACCCATCATGGAGAGCCCAAGTGTTCACAGCTGATGGCCACCCCGCTGCTGCTCACTACA 1392
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RESULT 7
BD123524LOCUS BD123524
DEFINITION Secretory protein or membrane protein.
ACCESSION BD123524
VERSION BD123524.1 GI:23218469
KEYWORDS JP 2002017376-A/33.2971 bp DNA
linear

PAT 18-SEP-2002

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QY	481	ATTGTCAATGCCCTCTCACCTCCTCAGCTGCGGCACCTTCGGCTTTTGTATCCGAAGTCCGGG	540
Db	493	ATTGCCAATGCCCTCTCACCTCCTCAGCTTGTGGCACCTTCGCTTTTGTATCCGAAGTCCGGG	552
QY	541	GTTATTGATGTGTCCAGTTTCCAGCAGGTTGAAAGACTTGAGAGCGGCCGCGGGGAAATGT	600
Db	553	GTTATTGATGTGTCCAGTTTCCAGCAGGTTGAAAGACTTGAGAGTGCCCGGGGGGAAATGT	612
QY	601	CTTTTGGAGCCAGCTCAACGGTCAGCAGCTGTAATGGCTGGGGGCTCCTCTACACCGCC	660
Db	613	CTTTTGGAGCCAGCTCAGCGGTGAGCAGCTGTAATGGCTGGGGGCTCCTCTATGCTGCC	672
QY	661	ACTGTGAAGAACTTCTGGGACTGAGCCCATCATCTCCCGAGCTGTGGGTGCGAGCTGAG	720
Db	673	ACTGTCAAAACTTACCTGGGAGCGAGCAATATATCACCAGAGCAGTGGGTGCGCGAG	732
QY	721	GACTGATTCGACAGAGACCTTGTCTATCCTGGCTTAATGCTCCAGCCTTTGTGCGAGCT	780
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QY	781	ATGGTCTCTGAGCCACGCTGAGTGGGGGATGAAGATGGAGAGCATGAAATCTTTTTC	840
Db	793	GTGGCTTTGAGCCAGCCCAATGGGGGGATGAAGATGGAGAGCACGAAATCTACTTCTTC	852
QY	841	TTACGAGACCTCCCGAGCTGTGGACTCTCTATGAGCGCATCAAGCTCCCAAGAGTGGCC	900
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QY	901	CGAGTGTGTGGGGGACCTTGGGGCAGGAAGACCCCTTACAGAGATGGAGAGCTTT	960
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QY	1261	CTCCAGCAGTTTGGATCCTCACTCTCCCTGCCAGACCGGGTGCACCTTTATCAGAGAC	1320
Db	1273	CTCCGGCAGCTTTGGGTCTACTCTCTCCCTGCTGACCGGCTACTCACCTTTCCTGGGAC	1332
QY	1321	CACCTCTCATGGACAGGCCGCTGTTCCTGGCTGACGGCGGCCCTGCTGTGCTACTACA	1380
Db	1333	CACCCACTCATGGACAGGCCAGTGTTCAGCTGATGGCCACCCCTGCTGTGCTACTACA	1392
QY	1381	GATACAGCCTATCTCAGAGTCTGTGGCCACAGGGGTGACAGCCTCTCAGGGGAAAGATAT	1440
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RESULT 9
BC038411
LOCUS

Homo sapiens, sema domain, immunoglobulin domain (19),
transmembrane domain (TM), and short cytoplasmic domain,
2948 bp mRNA linear PRI 02-OCT-2002
BC038411

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QY	2341	CCAAGCCAGCCCATCTCGGCTCAGTGGGGCGCTCTAGCCACGTGTGATGAGACCTCC	2400
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(semaphorin) 4F, clone MGC:34479 IMAGE:5179587, mRNA, complete cds.

ACCESSION
BC038411
VERSION
BC038411.1
KEYWORDS
MGC.
SOURCE
Homo sapiens (human)

GI:23468353

REFERENCE
AUTHORS
TITLE
JOURNAL

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2948)

Direct Submission

REMARK
COMMENT

Submitted (01-OCT-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgaps-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowls, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 51 Row: p Column: 3
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 19923278.

FEATURES
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CDS

602 a 834 c 836 g 676 t
Query Match 46.6%; Score 1867.8; DB 9; Length 2948;
Best Local Similarity 86.4%; Pred. No. 0;
Matches 2093; Conservative 0; Mismatches 312; Indels 18; Gaps 2;

BASE COUNT
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VERSION AX003081.1 GI:9926964
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Michalovich,D. and Doe,T.R.
TITLE Semaphorin family polypeptides and polynucleotides
JOURNAL Patent: EP 0933425-A 1 04-AUG-1999;
SMITHKLINE BEECHAM PLC (GB)
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Best Local Similarity 82.2%; Pred. No. 0;
Matches 2012; Conservative 0; Mismatches 319; Indels 117; Gaps 3;
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Db 35 GCCGAGGCCAGTAGCCCCGGGGCCCTGAGCAGAGGCCGTAGCTTGGCGCGCACCGCGCGC 94
QY 61 CAGCGGAGCCAGAGATGCTTGGCAGGGCCGAGCGGCCCGCCCGGGCGCCCGCGCGCT 120
Db 95 CAGCGGAGCCAAAGATGCCGGCTCTGCTGCGCGGCCCGCCCGGGGTCGGCGGCGAGCT 154
QY 121 CCGGTCTTCTCCCGCCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 155 ACAGCTCGCCCTTCCC-----GCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 199
QY 181 CCGGTGTGGCGCGCGTCCCGGCTCAGTGGCCAGAACCTCGCTGCGCCATCTCCGAGGCT 240
Db 200 CCGGTATCCGGCGCGCTCCCGGCTCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 259
QY 241 GACTCTATCTACCCGGTTCAGCGCTCTCATAGTACAATTAATCTGCTGCTGCTGCTGCTGCT 300
Db 260 GACTCTGCTCAGCCGGTTCGAGTCCCTCACATACAATTAATCTGCTGCTGCTGCTGCTGCT 319
QY 301 GATCTGCTCCCGCAGACTTTTACGTGCGTCAGCGGATAGCATCTTCGCTTTAAACCTC 360
Db 320 GATCTGCTCCCGCAGACTTTTATGTTGGCGCCCGGAGACCATCTTCGCTTTATCCCTG 379
QY 361 CCTTCTCTGGGGAAGACCCCGAGGATGCTGGATGTTACCTGAGACTCACAGACAG 420

Db	380	CCCTTCTCAGGGGAGAGACCCCAGAGTTGACTGTAGTGTTCTCGAGGCTCACAGACAG	439
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Db	881	TTGAAAGCTGACCTGCTCTCTCAGGGCTGAGCATGGCGGGCTCCAGTGTCTGCGAG	940
Qy	1021	GCTATGGCAGAGCTTCGGCTCAGCCTGGAGCGGGAACCCCCATCTTTTATGGATCTTT	1080
Db	941	GATGTTGCTGTGCTTCGACCTGAGCTTGGGCGAGGACTCCCATCTTTTATGGCATCTTT	1000
Qy	1081	TCCTCCAGTGGGAAGAGCTGCCATCTCTGCTGTGTGTGCTTCGACCCCAAGACATC	1140
Db	1001	TC TTCCAGTGGAGGGGGTACTATCTCTGCTGTCTGTGCTTCGACCCACCAAGACAT	1060
Qy	1141	CGGCACTGCTGAATGCTGCTTTTAGAGAGCTAAAACATGACTGCAACAGGGGACATGCCT	1200
Db	1061	CGGNACGTGCTGAATGCTGCTTCAGAGAACTAAAACATGACTGCAACAGAGAGCTGCCT	1120
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Qy	1261	CTCAGCAGTTTGGATCTCACHCTCCCTGCCAGACGGGTGCTCAGCTTTATCAGAGAC	1320
Db	1181	CTCCGGACATTTGGCTCATCTCTCCCTGCTGACCGCGTACTCACTCTCATCCCGGGAC	1240
Qy	1321	CACCTCTCATGACAGGCCCGGTTCGCCGCTGAGCGGCCCGCCCTGCTGGTCACTACA	1380
Db	1241	CACCCACTCATGACAGGCCAGTGTTTCCAGCTGATGGCCACCCCTGCTGGTCACTACA	1300
Qy	1381	GATACAGCTTATCTCAGAGTCTGGGCCACAGGGTGACACGCTCTCAGGGAAGAATAT	1440
Db	1301	GATACAGCTTATCTCAGAGTCTGGGCCACAGGGTGACAGCTCTCAGGGAAGAGTAT	1360
Qy	1441	GAGTGTCTTACCTGGGACAGAGATGGACACTCCACCGGCTGTGGCATTTGAGCT	1500

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Db	1541	ACCAACTGTGGCGCTCTCCAGAGCTGCTCAGAGTGATCTTGGCCAGGACCCAGTCTGT	1600
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Qy	1981	CAGGAGGTGTAGCGCCCGCGTGGTGGCTGTATTAGCTTTGTGTGGGACGCCAGCGG	2040
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Qy	2221	ACAAGCTATAGTCAGGACCTCCCTCTCCTTCCTGCGCTGAAGATGAACGGCTGCCCTGGCC	2280
Db	2138	ACAAGCTACAGCCAGACCCCTCCCTCCCTCTCCTGAAGATGAGCGGTTGCCGCTGGCC	2197
Qy	2281	CTGGGTAAAGCGGGCAGTGGTTTGTGGGCTTCCCTCCACCCCTTCTCTGTGGATCTTTC	2340
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ACCESSION BD177663			
VERSION BD177663.1 GI:30014925			

RESULT 11
BD177663
LOCUS
DEFINITION
ACCESSION
VERSION

[illegible]

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QY	721	GACTGATTCGACAGACAGACCTTGTATCTCTGGCTTAATGCTCCAGCCCTTTGTCGACGCT	780
Db	641	GACTGATTCGACAGACAGACCTTGTATCTCTGGCTTAATGCTCCAGCCCTTTGTCGACGCT	700
QY	781	ATGGTCTCTGAGCCCACTGAGTGGGGGATGAAGATGGAGACGATGAATCTTTTTC	840
Db	701	GTGGCTCTGAGCCCACTGAGTGGGGGATGAAGATGGAGACGATGAATCTTCTCTTC	760
QY	841	TTACGGAGACCTTCGGAGTGTGGACTCTATGAGCGCATCAAGTCCCAAGATGGGCC	900
Db	761	TTTACGGAGACTTCGGAGCATTTGACTCATACGAGCGCATTAAGATCCACGGGTGGCC	820
QY	901	CGAGTGTGCGGGGACCTTCGGGCGAGAGACCCCTTCACAGAGATGGACGCTTT	960
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QY	961	CTGAAGCTTGAAGCTGTGTGCCCCAGGGCCCGAGCATGGCCGGGCTTCGCGAG	1020
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QY	1021	GCTATGGCAGAGCTTCGGCCCTCAGCTTGAGCGGGAACCCCATCTTTTATGGGATCTTT	1080
Db	941	GATGTGTGTGCTTCGAGCTTGTGGGCGAGGACTTCCCATCTTTTATGGCATCTTT	1000
QY	1081	TCTCCAGTGGGAAGGAGCTGCCATCTCTGCTGTGTGCTTCGACCCCAAGACATC	1140
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Db	1181	CTCCGGCAGTTGGCTCATCTCTCTCCCTGCTGACCCGGTACTCACCCTTCATCCGGGAC	1240
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Job time : 14366.7 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 25, 2003, 19:18:34 ; Search time 7933.17 seconds
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12279.116 Million cell updates/sec

Title: US-09-284-180A-1

Perfect score: 4008

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
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6: em_estpl:*
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23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1585.2	39.6	2719	11 AK035993	AK035993 Mus muscu
2	1582	39.5	2855	11 AK047067	AK047067 Mus muscu
3	645	16.1	704	14 CB527136	CB527136 UI-M-FY0-
4	633.8	15.8	657	14 CB557408	CB557408 AMGNNUC:N

ALIGNMENTS

RESULT 1
AK035993
LOCUS
DEFINITION
AK035993 Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:9630025H20 product:sema domain, immunoglobulin domain (Ig), TM domain, and short cytoplasmic domain, full insert sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE

AK035993 2719 bp mRNA linear HTC 05-DEC-2002
Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:9630025H20 product:sema domain, immunoglobulin domain (Ig), TM domain, and short cytoplasmic domain, full insert sequence.
AK035993.1 GI:26084949
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374

5	632.6	15.8	691	12	BM944530
6	612.2	15.3	868	10	BG323723
7	610.2	15.2	701	14	CB245456
8	596.6	14.9	1154	12	BM462308
9	596.4	14.9	693	12	BM963828
10	586.2	14.6	901	13	BQ213659
11	573.8	14.3	765	12	B1823626
12	566.2	14.1	758	14	CB244307
13	557.6	13.9	733	10	AW953466
14	555.8	13.9	578	14	CB607655
15	554.2	13.8	669	10	BB628682
16	546.8	13.6	733	10	AW957134
17	509	12.7	520	14	CB715569
18	508.8	12.7	772	12	B1915256
19	495.2	12.4	769	13	BQ745165
20	475.6	11.9	578	12	B1344452
21	475.2	11.9	669	12	BG774505
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23	455.6	11.4	486	10	BE982860
24	441.8	11.0	466	12	B1275275
25	437.2	10.9	466	9	AW123399
26	424.2	10.6	434	10	BF393117
27	418.2	10.4	689	10	BF467265
28	409.8	10.2	418	10	BF392081
29	405.2	10.1	434	9	AW123577
30	402.2	10.0	616	14	BY731493
31	397.4	9.9	556	10	BE683223
32	393	9.8	444	13	BY290889
33	388.4	9.7	1045	10	BF734978
34	386.8	9.7	503	9	AA459837
35	382	9.5	666	13	B0058887
36	380	9.5	380	14	CB810579
37	379	9.5	749	12	BQ042411
38	375.2	9.4	522	10	BE667719
39	370.8	9.3	379	10	BF392173
40	366.4	9.1	368	10	BF415905
41	362.8	9.1	731	12	BQ042997
42	352.2	8.8	416	13	BY224521
43	346.6	8.6	396	13	BY203844
44	319.8	8.0	425	13	BY237710
45	314.4	7.8	365	14	CD355327

[illegible]

QY	778	GCTATGGTCTCAGCCACGCTGAGTGGGGGATGAAGATGAGACGATGAATCTTTT	837	DEFINITION	Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length
Db	816	GCTATGGTCTGAGCCGCTGAGTGGGGGATGAAGATGAGACGATGAATCTTTT	875	ACCESSION	AK047067
QY	838	TTCTTCACGGAGACCTCCCGAGTGTGGACATCTATGAGCGCATCAAGGTGCCAAGAGTG	897	VERSION	AK047067.1 GI:26091917
Db	876	TTCTTCACGGAGACCTCCCGAGTGTGGACATCTATGAGCGCATCAAGGTGCCAAGAGTG	935	KEYWORDS	HTC; CAP trapper
QY	898	GCCGAGTGTGTGCGGGGACCTTGGGGCAGGAGACCTTTCAGCAGAGATGACGACG	957	SOURCE	Mus musculus
Db	936	GCCGAGTGTGTGCGGGGACCTTGGGGCAGGAGACCTTTCAGCAGAGATGACGACG	995	ORGANISM	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
QY	958	TTTCTGAAGGTGACTGCTGTGCCAGGCGCCGAGCATGCGCGGCTCCGGGTTCTG	1017	REFERENCE	Carninci, P. and Hayashizaki, Y.
Db	996	TTTCTAAAGGTGACTGCTGTGCCAGGCGCCGAGCATGGAAGGGCTCGGGGTTCTG	1055	AUTHORS	High-efficiency full-length cDNA cloning
QY	1018	CAGGCTATGGCAGCTTCGGCCCTCAGCTCGAGCGGGAACCCCATCTTTATGGGATC	1077	JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
Db	1056	CAGGATATGACAGCTTCGACCTCAGCTCGCGGGGACCCCTCTTTATGGGATC	1115	MEDLINE	99279253
QY	1078	TTTTCTCCAGTGGGAAGGAGCTGCCATCTCTGTGTGCTTCGACCCCAAGAC	1137	PUBMED	10349636
Db	1116	TTTTCTCCAGTGGGAAGGAGCCCATCTTCTGTGTGCTTCGACCCCAAGAC	1175	REFERENCE	Carninci, P. and Hayashizaki, Y.
QY	1138	ATCCGGGAGTGTGAATGGTCCCTTTAGAGAGCTAAACATGACTCAACAGGGGACTG	1197	AUTHORS	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Db	1176	ATCCGGGAGTGTGAATGGTCCCTTTAGAGAGCTAAACATGACTCAACAGGGGACTA	1235	TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to
QY	1198	CTGTTCATGGACAACGAGTGCCCGACCCAGACCTGGAGAGTCATCGCCACACATG	1257	JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
Db	1236	CTGTTCATGGACAACGAGTGCCCGACCCAGACCTGGAGAGTCATCGCCACACATG	1295	MEDLINE	20493374
QY	1258	AAGCTCCAGCAGTTTGGATCTCTACTCTCCCTGCGACACCGCGTCACTTTATCAGA	1317	PUBMED	11042159
Db	1296	AAGTCCAGCAGTTTGGATCTCTACTCTCCCTGCGACACCGTGTCTTATCAGA	1355	REFERENCE	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
QY	1318	GACCACTCTCATGACAGGCCCTGTTCCTCCGGCTGACGGCGCCCTGCTGGTCACT	1377	AUTHORS	Konno, H., Akiyama, J., Nishi, K., Katsuna, T., Tashiro, H., Itoh, M.,
Db	1356	GACCACTCTCATGACAGGCCCTGTTCCTCCGGCTGACGGCGCCCTGCTGGTCACT	1415	JOURNAL	Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
QY	1378	ACAGATACAGCTATCTCAGAGTGTGGCCACACAGGTTGACAGCCTCTCAGGAAAGAA	1437	MEDLINE	Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Db	1416	ACGATACAGCTATCTCAGAGTGTGGCTCACCAGGTTGACAGCCTCTCAGGAAAGAA	1475	PUBMED	Fujwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
QY	1438	TATGAGTGTCTACCTGGGACAGAGATGGACACCTCCACCGGGTGTGCGATTTGA	1497	AUTHORS	Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Db	1476	TATGATGTCTACTCTGGGACAGAGATGGCACTCCATCGGGCTGTGCGATCGGA	1535	TITLE	OKazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
QY	1498	GTCAGCTCAGTGTCTTGAGAGATGCGCTTGTTCAGAACACACACCGGTTGAGAGC	1557	JOURNAL	RIKEN integrated sequence analysis (RISA) system--384-format
Db	1536	GCTCAGCTCAGTGTCTTGAGAGATGCGCTTGTTCAGAACACACACCGGTTGAAAGC	1595	MEDLINE	Genome Res. 10 (11), 1757-1771 (2000)
QY	1558	ATGAATTTACACAGATGCTCTGTGGGCTCCCATCTAGGTGACACAGTGAAC	1617	PUBMED	20530913
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QY	1618	ACCAGCACTGTGGCGCTCTCAGAGTGTCTGGAGTGTATCTGTGGCCAGACCCGCTG	1677	AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Db	1656	ACCAGCACTGTGGCGCTCTCAGAGTGTCTGGAGTGTATCTGTGGCCAGACCCGCTG	1715	JOURNAL	Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
QY	1678	TGCGCTGGAGCTTCGGCTTGTATCTGTGTGGCCACCGCGCGGAGCCGCGGATG	1737	MEDLINE	Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
Db	1716	TGCGCTGGAGCTTCGGCTTGTATCTGTGTGGCCACCGCGCGGAGCCGCGGATG	1775	PUBMED	Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
QY	1738	GT 1739		AUTHORS	Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Db	1776	GT 1777		TITLE	Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
QY	1776	GT 1777		JOURNAL	Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G.,
Db	1776	GT 1777		MEDLINE	Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M.,
QY	1776	GT 1777		PUBMED	Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Db	1776	GT 1777		AUTHORS	Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
QY	1776	GT 1777		JOURNAL	Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,
Db	1776	GT 1777		MEDLINE	Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
QY	1776	GT 1777		PUBMED	Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,
Db	1776	GT 1777		AUTHORS	Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
QY	1776	GT 1777		TITLE	Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Db	1776	GT 1777		JOURNAL	Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,
QY	1776	GT 1777		MEDLINE	Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilm, L.,
Db	1776	GT 1777		PUBMED	Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
QY	1776	GT 1777		AUTHORS	and Hayashizaki, Y.
Db					

RESULT 2
AK047067
LOCUS

TITLE		Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-722 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)	
JOURNAL		cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	
FEATURES		Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/ Location/Qualifiers 1. .2855 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM_DB:B930015M09" /db_xref="taxon:10090" /clone="B930015M09" /tissue_type="cerebellum" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="10 days neonate". 1. .2855 /note="sema domain, immunoglobulin domain (Ig), TM domain, and short cytoplasmic domain (MGD MG1:1340055, GB NM_011350, evidence: BLASTN, 99%, match=1662)"	
BASE COUNT	580 a	795 c	746 g 733 t 1 others
ORIGIN			
Query Match 39.5%; Score 1582; DB 11; Length 2855; Best Local Similarity 94.7%; Pred. No. 1.1e-175; Matches 1649; Conservative 0; Mismatches 90; Indels 3; Gaps 1;			
Qy	1	GCCAGGCCCGCAGTAGGCGTACTAAGTAGAGGCTGTGGAGCGCGCCACCCGGGAC	60
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Qy	61	CAGCGGAGCGCAGAGATGCTTGCAGGGCGAGCGGCCGCCCGCGCGCCCGCGCGCT	120
Db	80	CAGCGGAGCGCAGAGATGCTGGCCAGGGCGAGCGGCCGCCCGCGCGCCCGCGCT	139
Qy	121	CCGCTCTTCCCTTCCCGCGCGCGCTCTCGGTG---CTGCTGCTGCTGGCGATACTAAGC	177
Db	140	CCGCTCTCTCTTTCCTCCCGCGCGCGCTCTGCTGCTGCTGCTGCTGGCGATCTGAGC	199
Qy	178	GCCCGGTGTGGCGCGCGCTGCCCGCTCAGTGCCCAAGACCTCGCTGCCCATCTCCGAG	237
Db	200	GCCCGGTGTGGCGCGCGCTGCCCGCTCAGTGCCCAAGACCTCGCTGCCCATCTCCGAG	259
Qy	238	CGTGACTCTATCTCACCCGGTTGACGCTCTCATACGTACATTTACTCTGCTCTCCTT	297
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Qy	298	GTGGATCCTGCCTCCACACACTTTAGCTCGGTGCACGGGATAGCATCTTCGCTTTAAC	357
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Qy	358	CTCCCTTCTCTGGGAAAGACCCCGAAGATCGACTGGATGGTACCTGAGACTCACAGA	417
Db	380	CTGCCCTTCTCTGGGAAAGACCTCGAAGATCGACTGGATGGTGGCCGAGACTCACAGA	439

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Qy 1498 GCTCAGCTCAGTCTCTGGAGGATCTGGCCCTGTGTTCCAGAACACACAGCCGGTTGAGAGC 1557
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Qy 1558 ATGAAATTTGTACACAGATTTGGCTCTGGTGGCTCCCATAGTGAAGTGAAC 1617
Db 1580 ATGAAATTTGTACACAGATTTGGCTCTGGTGGCTCCCATAGTGAAGTGAAC 1639

Qy 1618 ACCAGCAACTGTGGCCCTCTCCAGAGCTGCTCGGAGTGTATCTCGGCCAGGACCCCGTG 1677
Db 1640 ACCAGCAACTGTGGCCCTCTCCAGAGCTGCTCGGAGTGTATCTCGGCCAGGATCCCGTG 1699

Qy 1678 TGCCTCTGGAGCTTCCGGCTTGATGCTGTGTGTCGCCACACCGCCGAGACCCGCGGATG 1737
Db 1700 TGTCCCTGGAGCTTCCGGCTTGCATGCTGTGTGTCGCCATGACGAGCGACCCGTGGGTGA 1759

Qy 1738 GT 1739
Db 1760 GT 1761

RESULT 3
CB527136
LOCUS CB527136 704 bp mRNA linear EST 28-MAR-2003
DEFINITION UI-M-FY0-cfh-i-24-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
IMAGE: 6849601 5', mRNA sequence.
ACCESSION CB527136
VERSION CB527136.1 GI:29360609
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
1 (bases 1 to 704)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NTH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.
FEATURES
source Location/Qualifiers
1..704
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE: 6849601"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dp"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FY0"
/note="Organ: Brain; Vector: pYX-Asc; Site_1: Ecor I;
Site_2: Not I; The library was constructed according
Ronald, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCAGACAGAC. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Henin Chin, Ph.D.,

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BASE COUNT 149 a 180 c 212 g 163 t
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Query Match 16.18; Score 645; DB 14; Length 704;
Best Local Similarity 95.68; Pred. No. 3.3e-66;
Matches 674; Conservative 0; Mismatches 30; Indels 1; Gaps 1;
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Qy 440 AGAAGAGGAGCAATGTCAAAATTTATCCAGATTCGCGCATTTGTCAATGCCCTCTCACC 499
Db 61 AGAAGAGGAGCAATGTCAAAATTTATCCAGATTCGCGCATTTGTCAATGCCCTCTCACC 120
Qy 500 TCCTCAGCTGCGGACCTTCGCTTTTGTATCCGAGTGGCGGTTATTTGATGTGCCAGTT 559
Db 121 TCCTCAGCTGCGGACCTTCGCTTTTGTATCCGAGTGGCGGTTATTTGATGTGCCAGTT 180
Qy 560 TCCAGCAGGTTGAAAGACTTGAGAGCGCCGCGGGAATATGCTCTTTTTCAGCCAGCTCAAC 619
Db 181 TCCAGCAGGTTGAAAGACTTGAGAGTGGCCGCGGGAATATGCTCTTTTTCAGCCAGCTCAAC 240
Qy 620 GGTCAAGCAGCTGTAATGGCTGGGCGCTCTCTACACGCGCACTGTGAAGAACTTCCTGG 679
Db 241 GGTCAAGCAGCTGTAATGGCTGGGCGCTCTCTACACGCGCACTGTGAAGAACTTCCTGG 300
Qy 680 GGTCAAGCAGCTGTAATGGCTGGGCGCTCTCTACACGCGCACTGTGAAGAACTTCCTGG 739
Db 301 GGTCAAGCAGCTGTAATGGCTGGGCGCTCTCTACACGCGCACTGTGAAGAACTTCCTGG 360
Qy 740 CTTTGTCTATCTGCTGCTTAATGCTCGAGCTTTGTCGAGCTATGCTGAGCCAGCTGTG 799
Db 361 CTTTGTCTATCTGCTGCTTAATGCTCGAGCTTTGTCGAGCTATGCTGAGCCAGCTGTG 420
Qy 800 AGTGGGGGATGAAGATGGAGACGATGAAATCTTTTTTTTTCACGAGACCTTCCCGAG 859
Db 421 AGTGGGGGATGAAGATGGAGACGATGAAATCTTTTTTTTTCACGAGACCTTCCCGAG 480
Qy 860 TGTGGGACTCTATGAGCGCATCAAGTCCCAAGAGTGGCCGAGTGTGCGGGGAGCC 919
Db 481 TGTGGGACTCTATGAGCGCATCAAGTCCCAAGAGTGGCCGAGTGTGCGGGGAGCC 540
Qy 920 TTGGGGGAGGAGAACCCCTTCAGCAGAGATGGAGACGCTTTTCTGAAGGCTGACCTGCTGT 979
Db 541 TTGGGGGAGGAGAACCCCTTCAGCAGAGATGGAGACGCTTTTCTGAAGGCTGACCTGCTGT 600
Qy 980 GCCCAGGCGCCGAGCATGGCCGCGCTCCCGGGTTCTGACGCTATGCGAGAGCTTCGCGC 1039
Db 601 GTCCAGGCGCCGAGCATGGAAAGGCTCGGGGGTTCTGCAGGATATACAGAGCTTCGAC 660
Qy 1040 CTCAGCTGGAGCGGAGACCCCATCTTTTATGGATCTTTTCCT 1084
Db 661 CTCAGCTGGAGCGGAGACCCCATCTTTTATGGATCTTTTCCT 704

RESULT 4
LOCUS CB557408 657 bp mRNA linear EST 02-APR-2003
DEFINITION AMGNNUC:NRH3-00245-F12-A w Rat hypothalamus (10735) Rattus
norvegicus cDNA clone nrh3-00245-f12 5', mRNA sequence.
ACCESSION CB557408
VERSION CB557408.1 GI:29496808
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 657)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program

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|||||
241 AATGGCTGGGGCGTCTCTACACGCCCACTGTGAATAACTTCTCTGGGACAGAGCCGAT 300
QY CATCTCCCGAGCTGTGGTGGAGCTGAGGAGTTCGAACAGAGACCTTGTCACTCTG 752
Db TATCTCCCGAGCTGTGGTGGAGCTGAGGACTGGATTCGACAGAGACCTTGTCACTCTG 360
QY GCTTAATGTCAGCCTTTGTGCGAGCTATGTCCTGAGCCCACTGAGTGGGGGATGA 812
Db GCTTAATGCCACGCTTTGTGCGAGCTATGTCCTGAGCCCGCTGAGTGGGGGATGA 420
QY AGATGAGAGCATGAATCTTTTCTTTCACGGAGACCTCCGAGTGTGACACTCCTA 872
Db AGATGAGAGCATGAATCTTTTCTTTCACGGAGACCTCCGAGTGTGACACTCATA 480
QY TGAGCGCATCAAGGTCCCAAGAGTGGCCGAGTGTGTGCGGGGAGCTTGGGGGACAGAA 932
Db TGAGCGCATCAAGGTCCCAAGAGTGGCCGAGTGTGTGCGGGGAGCTTGGGGGACGAA 540
QY GACCTTTCAGCAGAGATGGACAGCTTTCTGAAGGTGACCTGTGTGCCAGGGCCGA 992
Db GACCTTTCAGCAGAGATGGACAGCTTTCTGAAGGTGACCTGTGTGCCAGGGCCGA 600
QY GCATGCGGGGCTCCGGGTTCTGAGGCTATGAGGAGCTTCGGGCTCAGCTGGAGC 1052
Db GCATGGAAGGCTCGGGGTTCTGAGGATATGACAGAGCTTCGACCTCAGCTGGCGC 660
QY 1053 GGGACCCCATCTTTTATGGGATCTTTTCT 1084
Db 661 GGGACCCCATCTTTTATGGGATCTTTTCT 691

RESULT 6
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LOCUS 868 bp mRNA linear EST 27-FEB-2001
DEFINITION 602421820F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4560028 5',
mRNA sequence.
ACCESSION BG323723
VERSION BG323723.1 GI:13130160
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 868)
AUTHORS NIH-MGC <http://mgi.nhl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
plate: LLC1268 row: g column: 05
High quality sequence stop: 860.
Location/Qualifiers
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/notes="Organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 167 a 240 c 273 g 188 t
ORIGIN
Query Match 15.3%; Score 612.2; DB 10; Length 868;
Best Local Similarity 83.4%; Pred. No. 1.9e-62;
Matches 721; Conservative 0; Mismatches 138; Indels 6; Gaps 2;
QY 1559 TGAATTTGTACACGATTTGGCTCTCTGGTGGCTCCCACTAGGTTGAGGTGACACAAAGTGAACA 1618
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Db 62 CAACCAACTGTGGCCGCTCTCCAGAGCTGTCTCGAGTGTATCTCTGGCCAGGACACCCCTGT 121
QY 1679 GCCTCTGGAGCTTCGCGCTTGTATGCTGTGTGGCCACGCGGGGAGCAGCCGGGATGG 1738
Db 122 GTGCTGGAGCTTCGCGCTGATGATGTGTGGCCATGTGGCCATGTGGCCGAGCAGCGGGTGG 181
QY 1739 TTCAAGATATAGAGTCAAGCGATCTCTCTTCTTGTCTCCAAAGAACCTGGAGAACATC 1798
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QY 1799 CCCTAGTGTGTAAGTTCCCGTGGCTACTGTGGCCACAGCTGGTCTCTGCCATGTTCCCCCA 1858
Db 242 CAGTAGTGTGTAAGTTCCCGTGGCTACTGTGGCAGCTGGCATGTGTCTTCCCATGTTCTCAA 301
QY 1859 GTTCTGCTGGGATCCTGTGTGTGGCACCAGCCAGTGTGAGTGTACTCTACTCTCTCTCTCT 1918
Db 302 GCTCAGCATGGGATCCTGTGTGTGGCACCAGCCAGTGTGAGTGTACTCTACTCTCTCTCTCT 361
QY 1919 GGAGGGATGACATAGAGTGTGTGTGACCCAGGCGGCTATGAGTGTGGGCTTATGCTTGCAGT 1978
Db 362 GCGGGATGACATAGAGTGTGTGTGACCCAGGCGGCTATGAGTGTGGGCTTATGCTTGTGAAT 421
QY 1979 GTCAGGAGGTGGAGCGCGCGCTGTGTGTGTATAGCTTGTGTGGGCGGACGCGAC 2038
Db 422 GTCAGGAGGTGGGCGGCGGCTGT 481
QY 2039 GGGAGCCCTCAACCGGCGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2098
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QY 2099 GTCTTCTTGCAGCATCCT 2158
Db 540 GGATTTCTGCAGCATCCT 599
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QY 2219 CCACAAAGTATAGTACAGGACCCCT 2278
Db 660 CCACAAAGTATAGTACAGGACCCCT 719
QY 2279 CCCTGGGTAAAGCGGGGAGT 2338
Db 720 CCCTGTCAAGAGGGGAGT 779
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QY 2399 CCATCTAAAGCGGGGAGAAATGACT 2423
Db 836 CCATCTAAAGCGGGGAGAAATGACT 860

[illegible]

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 02:11:50 ; Search time 620.263 seconds
(without alignments)
8552.073 Million cell updates/sec

Title: US-09-284-180A-1

Perfect score: 4008

Sequence: 1 gccgagccgcgcagtagc.....aaaaaaaaaaaaaaaaaaaa 4008

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1152032 segs, 561743493 residues

Total number of hits satisfying chosen parameters: 2304064

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	1283	32.0	2082	1	PCT-US03-27411-47
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3	248.6	6.2	1914	1	PCT-US03-09929-7
4	248.6	6.2	1914	1	PCT-US03-09929-9
5	247.8	6.2	3112	1	PCT-US03-09929-5
6	246	6.1	2739	1	PCT-US03-09929-11
7	223.2	5.6	2049	1	PCT-US03-09929-3
8	215.2	5.4	2589	1	PCT-US02-36071A-168
9	215.2	5.4	4157	1	PCT-US02-36071A-167
10	205.6	5.1	2586	1	PCT-US02-36071A-165
11	205.6	5.1	2769	1	PCT-US02-36071A-164
12	155.6	3.9	2705	1	PCT-US03-27411-44
13	145	3.6	725	1	PCT-US03-27411-40
14	69.2	1.7	19290	7	US-60-500-337-19393
15	69.2	1.7	46339	7	US-60-500-337-19384
16	66.6	1.7	32874	1	PCT-US02-36071A-154
17	66.2	1.7	96595	1	PCT-US02-38582-43
18	65.2	1.6	349443	5	US-09-947-914-47
19	65	1.6	201	7	US-60-487-610-23416
20	65	1.6	60321	7	US-60-485-450-15208
21	65	1.6	2027	1	PCT-US02-36071A-187
22	64.6	1.6	66843	8	US-60-500-337-19683
23	64.4	1.6	450000	6	US-10-650-449-3
24	64.2	1.6	55492	7	US-60-487-610-19542
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26	64.2	1.6	56144	7	US-60-495-135-3633

Sequence 169, App
Sequence 53, Appl
Sequence 5203, Ap
Sequence 64272, A
Sequence 19632, A
Sequence 12090, A
Sequence 31, Appl
Sequence 2607, Ap
Sequence 2629, Ap
Sequence 2651, Ap
Sequence 2673, Ap
Sequence 2889, Ap
Sequence 2711, Ap
Sequence 2733, Ap
Sequence 14691, A
Sequence 21318, A
Sequence 81685, A
Sequence 81691, A
Sequence 19240, A

ALIGNMENTS

RESULT 1

PCT-US03-27411-47
; Sequence 47, Application PC/TUS0327411
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; Lee, Soo Yeun;
; APPLICANT: ELLIOTT, Vicki S.; HAFALIA, April J.A.;
; APPLICANT: BURFORD, Neil; SPRAGUE, William W.;
; APPLICANT: GRIFFIN, Jennifer A.; YANG, Yonghong G.;
; APPLICANT: CHAWLA, Narinder K.; BAUGHN, Mariah R.;
; APPLICANT: BECHA, Shanya D.; KHARE, Reena;
; APPLICANT: THORNTON, Michael B.; MASON, Patricia M.;
; APPLICANT: GIETZEN, Kimberly J.; ISON, Craig H.;
; APPLICANT: RAMQUIS, Joseph P.; SWARNAKAR, Anita;
; APPLICANT: RICHARDSON, Thomas W.; TRAN, Uyen K.
; TITLE OF INVENTION: NEUROTRANSMISSION-ASSOCIATED PROTEINS
; FILE REFERENCE: PF-1557 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/27411
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/408,383
; PRIOR FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 60/408,781
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/414,221
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/426,483
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 60/431,566
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/434,317
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 60/437,763
; PRIOR FILING DATE: 2003-01-03
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PERL Program
; SEQ ID NO 47
; LENGTH: 2082
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No: 7523644CB1
PCT-US03-27411-47

Query Match 32.0%; Score 1283; DB 1; Length 2082;
Best Local Similarity 82.5%; Pred. No. 0;
Matches 1546; Conservative 0; Mismatches 215; Indels 114; Gaps 2;
Qy 61 CAGCGGAGCAGAGATGCTTGCCAGGGCCCGCCCGCCGCGCT 120


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; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/372,002
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/386,816
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/389,123
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 60/402,207
; PRIOR FILING DATE: 2002-08-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 1
; LENGTH: 1914
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1908)
; PCT-US03-09929-1

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	Query Match	6.2%	Score 248.6;	DB 1;	Length 1914;
	Best Local Similarity	52.1%;	Pred. No. 1.5e-56;		
	Matches	704;	Conservative	0; Mismatches 629;	Indels 18; Gaps 6;
QY	383	GAAGGATCGACTGGATGGTACCTGAGACTCACAGACAGAAGAAAGGCAAG-	441		
Db	200	GAGCGATCTCTGGGAGGCCCGTGAGGAGAGAGACTGAGTGTATCCAGAAAGGGA	259		
QY	442	--AAAGAGGACGAATGTCACAATTATTTATCCAGATTTCTGCGCCATTGTGCAATGCCTCACC	499		
Db	260	ACAACACAGACCGAGTGTCTCACTTCATCCGCTTCCTGCAGCCCTCAATATGCTCCOAC	319		
QY	500	TCCTCAAGTCGGCACCTTCGCTTTTTGATCCGAAGTCGGGGTTATTGATGTCTCCAGTT	559		
Db	320	TGTACGTCCTGGCACCTACGCCTTCAGGCCAAGTGCACCTACGTCAACATGCTCACCT	379		
QY	560	TCGA---CGAGTTGAAGACTTTGAGAGCGCGCGGGGAATGTCTTTTGAAGCCAGCTC	616		
Db	380	TCACTTTGGAGCATGGAGAGTTTCAAGATGGGAAGGCAAGTGTCTTATGATGCCAGCTA	439		
QY	617	AACGGTCAGACGCTGTAATGCTGGGGGCTCTCTACACGCCACCTGTGAAGACTTCC	676		
Db	440	AGGGCCATGCTGGCTTCCTTGTGGATGGTGAGCTGTACTCGGGCACACTCAACAACCTCC	499		
QY	677	TGGGGACTGAGCCCATCATCTCCCGAGCTGTGGTGCAGCTGAGGACTGATTCGAACAG	736		
Db	500	TGGCAGGGAACCATATATCTCGGTANACATGGGCG---CCCACCCTCATGAAGACAG	556		
QY	737	AGACCTTGTTCATCTCGCTTAATGCTCCAGCCTTTGTGCGAGCTATGTCCTGAGCCAG	796		
Db	557	AGTACCTGGCCTTTTGGCTCAACGAACCTCACITTTGTAGGCTCTGCCTATGTACCTGAGA	616		
QY	797	CTGAGTGGGGGATGAAGATGGAGACATGAATCTTTTTTTTCTTCACGGAGACTTCCC	856		
Db	617	GTGTGGGCACCTTTCACGGGGGAGACACAAAGGTCTACTTCTTCTTCAGGGCGGGCAG	676		
QY	857	GAGTGTGGACTCTATGACCGCATCAAGTGTCCAAGATGGCCCGAGTGTGTGCGGGGG	916		
Db	677	TGGAGTCCGACTGCTATGCCGACAGTGTGTGCTGTGTGGCCCGTGTCTGCAAGGGCG	736		
QY	917	ACCTTTGGGGCAGGAAGACCTTTCAGCAGAGATGGACAGCTTTTCTGAAGGCTGACCTGC	976		
Db	737	ATATGGGGGGCAGCGACCCCTCGAGAGGAAGTGGACACAGCTTCTGTAAGGCCGCGGTGG	796		
QY	977	TGTGCCAGGCCCCGAGCATGGCCGGGCTCCGGGGTTCTGACGGTATATGGCAGAGCTTC	1036		
Db	797	CATGCTCTGCCCGAACTGSCAGCTCTACTTCAACCAGCTGCAGGGCATG---CACACC	853		
QY	1037	GGCCTCAGCTGGAGGGGAACCCCATCTTTTATGGATCTTTTCTCCCTCCAGTGGGAAG	1096		

Db	854	TGCAGGACACCTCTCTGGGACAAACACCACTCTCTTTGGGGTTTTTCAAGACACAGTGGGGT	913
Qy	1097	GAGCTGGCCATCTCTGCTGTGTGCTTCCGACCCCAAGACATCCGGGCACTGCTGAATG	1156
Db	914	ACATGTACCTGTGGCCATCTGTGAGTACCAGTTTGGAGAGATCCACGGGTGTTCGAGG	973
Qy	1157	GTCCCTTTAGAGACTAAACATGACTGCAACAGGGGACTGCCTGTTCATGGACAAACGAGG	1216
Db	974	GCCCTATAAGAGTAGCATGAGGAAGCCCAAGAGTGGGACCGCTACACTGACCCT--G	1030
Qy	1217	TGCCCCAGCCAGACCTTGGAGAGTGCATCGCCCAACATGAAGCTCCAGCAGTTTGGAT	1276
Db	1031	TACCCAGCCCTTGGCCCTGGCTGTGTCATTAACAACCTGGCATCGCGGCGCATACCA	1090
Qy	1277	CCTCACTCTCCCTGCCAGACCGCTGTCTACCTTTATCAGAGACCAACCCCTCTCATGGACA	1336
Db	1091	GCTCCCTGGAGCTACCCGACAAATCCTCAACTTCGTCAAGAAGCACCCGCTGATGGAGG	1150
Qy	1337	GGCCGCTGTTCCCGGCTGACGGCGCGCCCTGTCTGTGTCATCAGATACAGCCTATCTCA	1396
Db	1151	AGCAGTGGGGCTTCGGTGGAGCGCGCCCTGTCTGTGAAGAAGGGACCAACTTCAACC	1210
Qy	1397	GAGTCGTGGCCACAGGCTGACCAAGCCTCTCAGGGAAGAATATGACGTGCTCTACCTGG	1456
Db	1211	ACCTGGTGGCCGACGGGTTACAGAGCTTGATGGAGCCACTATACAGTGCCTGTTCAATG	1270
Qy	1457	GGACAGAGATGGACACTCCACCGGGCTGTGCCATTTGGAGCTCAGCTGCTCTTGG	1516
Db	1271	GCACAGGAGCGCTGGCTGCTCAAGGCTGTGAGCCTGGGCGCTTCACTGATG	1330
Qy	1517	AGGATCTGGCTTGT--CCAGAACACACAGCGGTGAGAGCATGAAATGTGACACG	1573
Db	1331	AGGAGCTGCAGCTGTTGACCAAGAGCCCATGAGAAGCCTGGTCTATCTCAGAGCAAGA	1390
Qy	1574	ATTGGCTCCTGGTGGCTCCACTACTGAGGTGACACAAAGTCAACACAGCAACTGTGGCC	1633
Db	1391	AGCTGCTCTTTGCCGGCTCCCGCTCTCAGCTGGTGACGCTGCCGTGGCGGACTGCATGA	1450
Qy	1634	GTCTCCAGAGCTGCTCGAGTGTATCTTGGCCAGAGACCCCGTGTGGCGCTGGAGCTTCC	1693
Db	1451	AGTATCGCTCTCTGTGCAGACTGTCTCTCGCCGGGACCCCTATTGCGCTGGAGCGTCA	1510
Qy	1694	GGCTTGATGCTTGTGGCCACCGCCGCGCA	1724
Db	1511	ACACGAGCGCTGTGTGGCCGTGGGTGGCCA	1541

RESULT 3

PCT-US03-09929-7

; Sequence 7, Application PC/TUS0309929

; GENERAL INFORMATION:

; APPLICANT: Curagen Corporation, et al.

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, A

; FILE REFERENCE: 21402-573B-061

; CURRENT APPLICATION NUMBER: PCT/US03/09929

; CURRENT FILING DATE: 2003-04-01

; PRIOR APPLICATION NUMBER: 60/368,996

; PRIOR FILING DATE: 2002-04-01

; PRIOR APPLICATION NUMBER: 60/369,980

; PRIOR FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: 60/370,381

; PRIOR FILING DATE: 2002-04-05

; PRIOR APPLICATION NUMBER: 60/370,969

; PRIOR FILING DATE: 2002-04-08

; PRIOR APPLICATION NUMBER: 60/371,002

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/372,002

; PRIOR FILING DATE: 2002-04-12

; PRIOR APPLICATION NUMBER: 60/384,297

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: 60/386,816

; PRIOR FILING DATE: 2002-06-07

; PRIOR APPLICATION NUMBER: 60/389,123

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RESULT 4
PCT-US03-09929-9
; Sequence 9, Application PC/TUS0309929
; GENERAL INFORMATION:
; APPLICANT: Curagen Corporation, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, A
; FILE REFERENCE: 21402-573B-061
; CURRENT APPLICATION NUMBER: PCT/US03/09929
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: 60/368,996
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/369,980
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/370,969
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/372,002
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/386,816
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/389,123
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 60/402,207
; PRIOR FILING DATE: 2002-08-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: Curaseq1ist version 0.1
; SEQ ID NO 9
; LENGTH: 1914

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1914)
PCT-US03-09929-9

Query Match 6.2%; Score 248.6; DB 1; Length 1914;
Best Local Similarity 52.1%; Pred. No. 1.5e-56;
Matches 704; Conservative 0; Mismatches 62; Indels 18; Gaps 6;

QY 383 GAAGATCGACTGGTGTACTGAGACTCAGACAGAACTGCAGGAGAAAGCACAAGA 442
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 200 GAGCGATCTCTGGGAGCCGCCCGTGGAGAAAGAACTGAGTGTATCCAGAAAGGGAAGA 259
443 A---AGAGGAGCAATGTACAAATTTATCCAGATTCTGCCATTGTCAATGCTCTCACC 499
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 260 ACAGCCAGACGAGTGTCAACTTCATCCGCTTCTCGACGCCCTACAAATGCTCTCCACC 319
500 TCCTCACGTGGGACCTTCGCTTTTGATCCGAAGTGGGGGTTATTGATGTGCCAGTT 559
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 320 TGTACGTCTGTGGCACCTACGCTTCCAGGCCAAGTGCACCTACGTCAACATGCTCACCT 379
560 TCCA---CGAGTTGAAGACTTGAGACGGCGGGGGGAATATGCTTTTGAGCCAGCTC 616
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 380 TCACCTTTGGAGCATGGAGAGTTTGAAGATGGGAAGGCAAGTGTCCCTATGACCCAGCTA 439
617 AACGTCAGCAGCTGTAATGCTGGGGCGTCTCTACACGCCCACTGTGAAGACTTCC 676
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 440 AGGCGCATCTGGCCCTCTTGTGGATGTGAGCTGTACTCGGCCACACTCAACAATTTCC 499
677 TGGGACTGAGCCCATCATCTCCGAGCTGTGGGTGAGCTGAGGACTGGATTTCGAACAG 736
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 500 TGGGCACGAACCATATTCTCGCTAACATGGGCG---CCACACACTCCATGAAGACAG 556
737 AGACCTTGTATCTCGCTTAATGCTCCAGCTTTGTGCGAGCTATGTCCTGAGCCACAG 796
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 557 AGTACCTGGCCCTTTTGGTCAACGAACCTCTTTGTAGGCTCTGCCCTATGACCTGAGA 616
797 CTGAGTGGGGGATGAAGATGAGACGATGAAATCTTTTCTTCAAGGAGACTCC 856
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 617 GTGTGGGAGCTTCACGGGGACGACGACAGGCTACTTCTTCAAGGAGCGGGGAG 676
857 GAGTGTGGACTCTTATGAGCGCATCAAGGTCCCAAGAGTGCCCGAGTGTGTGGGGGG 916
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 677 TGGAGTCGAGCTGTATCCGAGCAGGTGGTGGCTCGTGTGGCCCGTGTGCAAGGGCG 736
917 ACCTTGGGGGAGGAGACCTTCAGCAGAGATGGACGACGTTTCTGAAGCTGACCTGC 976
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 737 ATATGGGGGGCGCAGGACCTTCAGAGGAAGTGGACCACTTCTGAAGCGCGGCTGG 796
977 TGTGCCCAGGCGCGAGCATGGCCGGGCTCCGGGTTCTCAGGCTATGCGACAGCTTC 1036
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 797 CATGCTGTCCCCGACTGGGAGCTCTACTTCAACCACTCGAGGGGATG---CACACC 853
1037 GGCTTCAGCTGGAGCGGGAACCCCATCTTTTATGGGATCTTTTCTCCAGAGTGGGAAG 1096
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 854 TGCAGGACACCTCTCTGGCACAACACCACTTCTTTGGGGTTTTCACGACAGTGGGTG 913
1097 GAGTGCATCTCTGCTGTGTGCTTCGACCCCAAGATCCGGGCACTGCTGAATG 1156
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 914 ACATGTACTCTCGGCCACTGTGAGTACCAGTTTGAAGAGATCCAGCGGTTGTTGAGG 973
1157 GTCCTTTAGAGATAAAGATGACTGCAACAGGAGCTGCCCTGTCATGACACAGAGG 1216
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 974 GCCCTATAGAGTACCATGAGGAAGCCAGAGTGGGACCGCTACACTGACCT---G 1030
1217 TGCCCCAGCCAGACTGGAGAGTGCATCGCAACACATGAAGCTCCAGCAGTTTGGAT 1276
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1031 TACCAGCCCTCGGCCCTGCTCGTGCATTAAACACTGCGCATCGGGCGCCACGGCTACACCA 1090
1277 CCTCACTCTCCCTGCCAGCGGTGCTCACTTTATCAGAGACCACTCTCTATGGACA 1336
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1091 GCTCCCTGGAGCTACCCGACAACTCCTAACTTCGTCAAGAAGACACCCGCTGATGGAGG 1150
QY 1337 GGCCGCTGTCCCGGCTGACGGCGCCGCCCTGCTGCTCACTACATACAGCTTATCTCA 1396
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1151 AGCAGTGGGGCTCGGTGGAGCCGCCCTGCTGCTGAAGAGGGCACCACACTTCACCC 1210
1397 GAGTGTGGCCACAGAGTGACCGCTCTCAGGGAAGAAATATACGCTGTCTTACCTGG 1456
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1211 ACCTGTTGGCGGACCGGGTTACAGGACTTGATGGAGCCACCTATACAGTGTGTTTCATTG 1270
1457 GGACAGAGATGGACACCTCCACCGGGCTGTGCGGATTGGAGCTCAGCTCAGTGTCTGG 1516
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1271 GCACAGAGAGCGGTGGCTGCTCAAGGCTGTGAGCTGGGGCCCTGCGCTTACCTGATTTG 1330
1517 AGGATCTCGCCTTGT---CCAGAAACACAGCCGCTTGAGAGCATGAAATGTATCCAGC 1573
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1331 AGGAGCTCAGCTGTTTGACCAAGAGCCCATGAGAAGCCTGCTGCTATCTCAGACGAAGA 1390
1574 ATTGGCTCCTGTTGGGCTCCCATACTGAGGTGACAAAGTGAACACCAAGCAACTGTGGCC 1633
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1391 AGCTGCTCTTTGCCGCTCCGCTCTCAGCTGCTGAGTGGTGCAGTGGCCGCTGCATGA 1450
1634 GTCTCCAGAGCTGCTCGGAGTGTATCTTGGCCACGACCCCGTGTGCGCTGGAGCTTCC 1693
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1451 AGTATCGCTGTGTCAGACTGTGCTCTCGCCCGGACCCCTATTTCGCGCTGGAGCGTCA 1510
1694 GCCTTGATGCTTGTGTGGCCACGCGCGCA 1724
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1511 ACACGAGCGCTGTGTGGCCGTGGTGCGCA 1541

RESULT 5

PCT-US03-09929-5
; Sequence 5, Application PC/TUS0309929
; GENERAL INFORMATION:
; APPLICANT: Curagen Corporation, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND MET
; FILE REFERENCE: 21402-573B-061
; CURRENT APPLICATION NUMBER: PCT/US03/09929
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: 60/368,996
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/369,980
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/370,969
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/372,002
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/386,816
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/389,123
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 60/402,207
; PRIOR FILING DATE: 2002-08-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 5
; LENGTH: 3112
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104)..(2602)
PCT-US03-09929-5

Query Match 6.2%; Score 247.8; DB 1; Length 3112;

Best Local Similarity 52.18; Pred. No. 3.5e-56;		Matches 702; Conservative 0; Mismatches 627; Indels 18; Gaps 6;	
QY	387	GATCGACTGGATGGTACTGAGACTCACAGACAGAACTGCAGGAAGAAGAGCGAAG---AA	443
Db	361	GATCTCTGGGAGGCCCGCTGGAGAGAGAGACTGATGTATCCAGAAAGGGAGAACAA	420
QY	444	AGAGGACGAATGTCACAAATTTATTCAGATTCTGCCAATTGTCAATGCCCTCTCACCTCCCT	503
Db	421	CCAGACCGAGTGGCTTTCAACTTCATCCCGCTCTCTGCAGCCCTACAATGCCCTCCACCTGTA	480
QY	504	CAGCTGGGACACCTTCGCTTTTGATCCGAAGTGGGGGGTTATTGATGTGTCAGTTCCCA	563
Db	481	CGTCTGTGGCACCTTACGCCCTTCAGGCCCAAGTGCACCTAGGTCAACATGCTCACTTTCA	540
QY	564	---CGACGTTGAAGAGCTTGAGAGCGCCCGGGGAAATGTCTTTTCAGCCAGCTCAACG	620
Db	541	TTTGGACGATGGAGAGTTTGAAGATGGGAAGCGAGTGTCCCTATGACCCAGCTAAGGG	600
QY	621	GTGACGAGCTGTAAATGGCTGGGGCGTCTCTACACGCCCACTGTGAAGAACTTCCTGGG	680
Db	601	CCATGCTGGCTTCTTGTGGATGGTAGCTGTACTCGGCCACACTCAACAACATTCCTGGG	660
QY	681	GACTGAGCCCATCATCTCCGAGCTGTGGSTCGAGCTGAGGACTGGATTGCAACAGACAG	740
Db	661	CACGGAACCCATATCTCGGTAACTTGGGCG---CCACCACTCCATGAAGACAGAGTA	717
QY	741	CTTGTCACTCGGCTTAATGCTCCAGCGTTTGTGCGAGCTATGCTCTGAGCCAGCCAGCTGA	800
Db	718	CTTGGCTTTGGCTCAACGAACCTCACTTTGTAGGCTCTGCCCTATGCTAGAGTGT	777
QY	801	GTGGGGGATGAAGATGGAGACGATGAAATCTTTTTCCTCACGGAGACCTCCCGAGT	860
Db	778	GGGCAGCTTCAGGGGGACGACGACAGGTCTACTTCTTCTCAGGGGACGGCAGTGGA	837
QY	861	GTTGGACTCTATGAGCGCATCAAGTCCCAAGATGGCCCGAGTGTGTGCGGGGGACCT	920
Db	838	GTCCGACTGTATGCCGAGCAGGTGTGTGGTCTGTGTGGCCCGTCTCTGCAAGGGCGGAT	897
QY	921	TGGGGCGAGGAAGACCTTCAGCAGACATGGACGACGTTTCTGAAGGCTGACCTGCTGTG	980
Db	898	GGGGGGCGACGACCTTCAGAGGAAGTGGACCAAGTCTCCTGAGGCGGGCTGGCATG	957
QY	981	CCCAGGCCCGAGCATGGCCGGCCCTCCGGGGTCTCGAGGCTATGSCAGAGCTTCGGCC	1040
Db	958	CTCTGCCCGCAACTGGCAGCTACTTCAACACAGCTCGAGCGCATG---CACACCTGCA	1014
QY	1041	TCAGCTTGGAGGGGAACCCCATCTTTTATGGATCTTTTCTCCAGCTGGGAAGGAGC	1100
Db	1015	GGACACCTCTGGCACAACACCACTCTTTTGGGGTTTTTCAAGCAGAGTGGGTGACAT	1074
QY	1101	TGGCATCTCTGCTGTGTGCTTCCGACCCCAAGACATCGGGCAGTGTGTAATGGTCC	1160
Db	1075	GTACTCTGGCCATCTGTGAGTACCAGTTGGAGAGATCCAGGGGTGTTTGGGGCCC	1134
QY	1161	CTTTAGAGAGCTAAACATGACTGCACAGGGGACTGCCCTGTATGACAAACAGAGTGCC	1220
Db	1135	CTATAAGGAGTACCATGAGGAAGCCCAAGAGTGGGACCGCTACACTGACCT---GTACC	1191
QY	1221	CCAGCCGACAGCTGGAGATGTCATCGGCCACACATGAAGCTCCAGCAGTTTGGATCTC	1280
Db	1192	CAGCCCTTCGGCCTGTGTGTCATTAACAACCTGGCATCGCGCCAGCGGTACACCACTC	1251
QY	1281	ACTCTCCCTGCCAGACGGCTGTCACTTTATCAGAGACCACTCTCATGACAGGCC	1340
Db	1252	CTTGGAGCTACCCGACAACATCTCAACTTCGTCAAGAAGCAACCCGCTGATGAGGAGCA	1311
QY	1341	CGTGTTCCTCCGGCTGAGGCCGCCCTGCTGGTCACTACAGATACAGCTTATCTCAGAGT	1400
Db	1312	GGTGGGCCCTCGGTGGAGCGCCCTGCTGCTGTGGAAGAGGCAACCACTTCAACCACCT	1371
QY	1401	CGTGGGCCACAGGGTGACCAAGCTCTCAGGGAAGAATATGAGCTGCTTACCTGGGGAC	1460

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Db 1372 GGTGGCCGACCGGGTTACAGACATTGAGACCCACCTATACAGTGTGTTTCATTGGCAC 1431
QY 1461 AGAGATTGGACACCTCCACCGGCTGTGCGCATTTGGAGCTCAGCTCAGTGTCTTGGAGGA 1520
Db 1432 AGGAGACGGTGGCTGTCTCAAGGCTGTGAGCCTGGGCCCTTCACTGATTTGAAGA 1491
QY 1521 TCTGGCCCTTGT---CCAGAACACACAGCCGGTTTGAGAGCATGAAATTTGTACACGATTG 1577
Db 1492 GCTCAGCTGTGTTGACCAAGGAGCCCATGAGAAGCTTGGTATCTCAGAGCAAGAAGCT 1551
QY 1578 GCTCCTGGTGGGCTCCCATACTAGGTGACACAAAGTGAACACCAAGCAACTGTGGCCGCT 1637
Db 1552 GCTCTTTGGCGGCTCCCGCTCTCAGCTGTGTCAGCTGCCGTGGCCGACATGCAAGA 1611
QY 1638 CCAGAGCTGTCTGGAGTGTATCTCTGGCCAGGACCCGCTGTGCGCCTGGAGCTTCCGCG 1697
Db 1612 TCGTCTCTGTGCAGACTGTCTCTGCGCCGGGACCCCTATTGCGCCTGGAGCGTCAAC 1671
QY 1698 TGATGCTTGTGTGGCCACGCGCGCA 1724
Db 1672 CAGCCGCTGTGTGCGCGTGGGTGGCCA 1698

RESULT 6
PCT-US03-09929-11
; Sequence 11, Application PC/TUS0309929
; GENERAL INFORMATION:
; APPLICANT: Curagen Corporation, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND MET
; FILE REFERENCE: 21402-573B-061
; CURRENT APPLICATION NUMBER: PCT/US03/09929
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: 60/368,996
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/369,980
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/370,969
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/372,002
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/386,816
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/389,123
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 60/402,207
; PRIOR FILING DATE: 2002-08-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: Curaseq1 version 0.1
; SEQ ID NO 11
; LENGTH: 2739
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104)..(2602)
PCT-US03-09929-11

Query Match 6.1%; Score 246; DB 1: Length 2739;
Best Local Similarity 51.8%; Pred. No. 9.9e-56;
Matches 708; Conservative 0; Mismatches 640; Indels 18; Gaps 6;

QY 368 CTGGGAAACACCCCGAAGCATCGACTGGATGGTACTGTACCTGAGACTCAGACAGCACTGCA 427
Db 342 CTCGTGAGCTCGAAGGAGCATCTCTCTGGAGGCCCTCTCTGGAGAGCAAGACTGAGTGTA 401
QY 428 GGAAGAAGCAAG---AAAGAGGACGAATGTCCACAAATTTTATCCAGATTTCTCGCCATTG 484

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Db 440 TCACCTTTGAGCAGTGAGAGTTTGAAGATGGGAAGGCAAGTGTCCCTATGACCCAGCTA 499
QY 617 AACGGTCACAGCTGTAAATGGCTGGGGGGCTCTTACACCGCCACTGTGAAGAAGCTCC 676
Db 500 AGGGCCACTGCTGGCCTTCTTGTGGATGGTGAAGTGTACTTGGCCACACTCAACAAGTCC 559
QY 677 TGGGGACTGAGCCCATCATCTCCGAGCTGTGGGTGAGCTGAGGACTGGATTCGAACAG 736
Db 560 TGGGACGGAACCCATTATCTCGCTGAACATGGGGC---CCACACCACTCATGAAGACAG 616
QY 737 AGACCTTGCATCTCGGCTTAATGTCTCCAGCCTTTGTCCAGCTATGGTCTTGAGCCAG 796
Db 617 AGTACTGCCCCTTTTGGCTCAGCAACCTCACTTTGTAGGCTCTGCCTATGTACCTGAGA 676
QY 797 CTGAGTGGGGGATGAAGATGGAGCAGATGAATCTTTTTTCTTACGGGACACCTCC 856
Db 677 GTGTGGCAGCTTCACGGGGAGCAGCAGCAAGTCTACTTCTTTCAGGGAGCGGAG 736
QY 857 GAGTGTGACCTCTATGAGCGCATCAAGGTCCCAAGAGTGGCCGAGTGTGTGGGGGG 916
Db 737 TGGAGTCCGACTGCTATGCGAGCAGGTGGTGGCTGCTGTGGCCGCTGTCTGCAAGGGG 796
QY 917 ACCTTGGGGCAGGAGACCTTCACGACAGATGGACGACTTCTTGAAGGCTGACCTGC 976
Db 797 ATATGGGGGCGCAGCGCCCTGCAGAGGAAGTGGACACGTTCTTGAAGGCGCGGCTGG 856
QY 977 TGTGCCAGGGGCCGAGCATGGCCGGGCTCTCGGGGTTCTCGAGGCTATGCGAGAGCTTC 1036
Db 857 CATGCTCTGCCCGAAGTGGCAGCTACTTCAACACAGCTGACGGGATG---CACACC 913
QY 1037 GGCCTAGCCTGGAGGGGAAACCCCATCTTTATGGATCTTTTCTCCAGTGGGAAG 1096
Db 914 TGCAGGACACCTCTCGGCAACACACACCTTCTTTGGGTTTTCAGGACACAGTGGGGTG 973
QY 1097 GAGCTGCCATCTCTGCTGTGCTTCCGACCCCAACACATCCGGGAGTGCCTGAATG 1156
Db 974 ACATGTACCTGTGGCCCATCTGTGAGTACCACTTGGAGAGATCCAGCGGGTGTGAGG 1033
QY 1157 GTCCCTTTAGAGAGCTAAACATGATGCTCAACAGGGGAGTGCCTGTCTATGGACACGAGG 1216
Db 1034 GCCCTATAAGAGTACCATGAGGAAGCCAGAGTGGGACCGCTACACTGACCT---G 1090
QY 1217 TGCCTGAGCAGCTTGAGAGTGTGATGCGCAACATGAAGTCCAGCAGTTGGAT 1276
Db 1091 TACCCAGCCTCGGCTGCTGCTGATTAACACTGGCATCGGGGCCACGGCTACACCA 1150
QY 1277 CTTCACTCTCCCTGCGCAGACCGCTGCTCACCTTTATCAGACCAACCTCTCATGGACA 1336
Db 1151 GCTCCCTGAGGTACCCGAAACATCTCTCACTTCGTCAAGAACACCGCTGTGAGGAG 1210
QY 1337 GGCCTGCTGCTGAGCGCCGCCCTCTGCTGCTCACTACAGATACAGCCTATCTCA 1396
Db 1211 AGCAGTGGGGCTCGGTGGAGCCGCCCTCTCTGTAAGAGGCAACCACTTCACCC 1270
QY 1397 GAGTGTGCCCCACAGGTGACACCTCTCAGGGAAGAATATGAGTGTCTACCTGG 1456
Db 1271 ACCTGTGGCCGACCGGTTACAGGACTGTATGGAGCCACCTATACAGTGTCTCAATG 1330
QY 1457 GGACAGAGGATGACACCTCCACCGGCTGTGCGCATTTGGAGCTCAGCTGCTTGG 1516
Db 1331 GCACAGGAGACGGCTGGCAGCTCAAGGCTGTGAGCCTGTGGGCTTCACTGATG 1390
QY 1517 AGGATCTGGCCTTGT 1532
Db 1391 AGGAGCTGACGCTGT 1406

RESULT 8

PCT-US02-36071A-168

; Sequence 168, Application PC/TUS0236071A

; GENERAL INFORMATION:

; APPLICANT: Sagres Discovery

; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000142
; CURRENT APPLICATION NUMBER: PCT/US02/36071A
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 168
; LENGTH: 2589
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-36071A-168

Query Match 5.4%; Score 215.2; DB 1; Length 2589;
Best Local Similarity 48.9%; Pred.No. 2.3e-47;
Matches 747; Conservative 0; Mismatches 748; Indels 33; Gaps 5;
QY 211 CCAGAACCTCGCTGCCCATCTCCGAGGCTGACTCTATCTCACCCGGTTTGCAGGCTCT 270
Db 76 CCATATACCCCGGATCACCTGGGAGCACAGAGGTGCACCTGGTGAGTTTCATGAGCCA 135
QY 271 CATAGTACAATTAATCT 330
Db 136 GACATCTACAACT 195
QY 331 GCACGGGATAGCATCT 390
Db 196 GCCGGGAGGGGCT 255
QY 391 GACTGGATGCTACCTGAGACTCACAGACAACTGCAGGAAGAAAGGCAAG---AAAGAG 447
Db 256 TATTGGAAGTCTCAGAGACAAAAGCAAAATGTGCAGAAAAGGGAAATCAAAACAG 315
QY 448 GACGAATGTCAAAATTTATCCAGATTCGCGCATTTGTCATGCTCTCTCTCTCTCTCT 507
Db 316 ACAGAGTGCTCAAACTACATCCGGGTGCTGACGCCACTCAGGCCACTTCCCTTTACGT 375
QY 508 TCGGCACCTTCGCTTTTGTATCCGAAGTCGGGGTTATTGATGTGTCAGTTTCCAGCAG 567
Db 376 TGTGGACCAACGCAATTCACGCCGGCTGTGACCACTGAACCTTAACATCTCTTTAAGTTT 435
QY 568 GTTGAAGACTTTGAGAGCGCGGGGAAATTCCTTTTGGCCAGCTCAACGGTCAAGCA 627
Db 436 CTGGGAAAATGAAGATGGCAAGAGATGTCCCTTTGACCCAGCACAGCTACACA 495
QY 628 GCTGTAAATGGCTGGGGGCTCTCTACACCGCCACTGTGAAGAACTTCTCTGGGACTGAG 587
Db 496 TCCGTATGTTGATGGAGAACTTTATTCGGGGAGCTCGTATATTTTGGGAAGTGAA 555
QY 688 CCATCATCTCCGAGCTGTGGTGCAGCTGAGGACTGGATTCGAACAGAGACCTTGTCTCA 747
Db 556 CCATCATCTCCGAAATTTCTCCACAGCTCTCTGAGGACAGATATGCAATCC----- 610
QY 748 TCTGGCTTAATGCTCCAGCCTTTGTGCGAGCTATGTCCTGAGCCAGCTGAGTGGGG 807
Db 611 -CTTGGCTGAACGAGCTAGTTTCTGTTGTTGCTGAGCTGATCCGAAAAGCCAGACAGC 669
QY 808 GATGAAGTGGAGAGATGAATCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 867
Db 670 CCCGCGGAGGATGACAGGCTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 729
QY 868 TCCTATGAGCGCATCAAGTCCCAAGAGTGGCCCGAGTGTGTCGGGGGACCTTGGGGC 927
Db 730 TTTGTTCAGGGTCTGATCCAGGATGAGCAAGAGTGTGCAAGGGGACCGAGCGCGC 789
QY 928 AGGAAGACCTTTACGACAGATGGACAGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCT 987
Db 790 CTGAGGACCTTGCAGAAAGAAATGAGACCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 849
QY 988 CCCGAGCATGGCCGGGCTCTCGGGGTTCTGAGGCTATGGCAGAGCTTCCGGCTCAGCCT 1047

Db 850 CCAGACAGCGGCTTGGTCTTCAATGTGCTCGGGAATGCTTCTGCTCAGGTC---CCCG 906
Qy 1048 GGAGCGGGAACCCCACTCTTTTATGGATCTTTTCTCCAGTGGGAGGAGTGCATC 1107
Db 907 GGCTGAAGGTGCTGTGTCTATGCACTCTTCCACCCACAGCTGAACAACGTTGGGCTG 966
Qy 1108 TCTGCTGTGTGTGCC-----TTCCGACCCCAAGACATCCGGGCGAGTGCATGATGGT 1158
Db 967 TCGCAGTGTGCGCTTACACCTGTCCACAGCCGAGGAGTCTTCTCCACGGGAAGTAC 1026
Qy 1159 CCCTTTAGAGAGTAAACATGACTGCAACAGGGAGTGCCTGTCTATGGACAACAGAGTG 1218
Db 1027 ATGAGAGACCAACAGTGGAGCAGTCCACACCAAGTGGTGGCTATATATGCGCCGGTA 1086
Qy 1219 CCCAGCCAGACTGGAGAGTGCATCGCCCAACAACATGAAGCTTCAGCAGTTTGGATCC 1278
Db 1087 CCAAGCCGGGCTGGAGGTGCATCGACAGAGGAGCGAGCGGCGGCAACTACACAGC 1146
Qy 1279 TCACTCTCCCTGCGACACCGCTGCTCACCTTTATCAGAGCACCACTCTCATGGACAGG 1338
Db 1147 TCCTTGAATTTGCCAGACAGACGCTGCAGTTCGTTAAAGACCACTCTTGTATGATGAC 1206
Qy 1339 CCGGTGTTCCGGCTGACGGCCGCCCTGCTGCTGCTCACTACAGATACAGCCTATCTCAGA 1398
Db 1207 TCGGTAACCCCAATAGACAACAGGCCCGCAGGTTAATCAAGAAAGATGTGAACACTACCCAG 1266
Qy 1399 GTGTCGCCACAGGAGTGACACGCTCTCAGGGAAGAAATATGACGTGCTTACCTGGGG 1458
Db 1267 ATCGTGTGACCGGACCCAGGCCCTGGATGGGAGTGTCTATGATGTCATGTTGTGACG 1326
Qy 1459 ACAGAGGATGGACACCTCCACCGGGCTGTCGCAATGGAGCTCAGCTCAGTGTCTTGGAG 1518
Db 1327 ACAGCCGGGAGCTCTGCAACAAGCATCAGCCTCGAGCACGCTGTTACATCATCGAG 1386
Qy 1519 GATCTGGCCTTTCCAGAACACAGCCCGGTTGAGAGCATGAATTTGTA----- 1568
Db 1387 GAGACCCAGCTCTTCCAGGACTTTGAGCCAGTCCAGACCTGCTGTCTTCAAGAAG 1446
Qy 1569 --CCAGATTGGCTCTGTGGGCTCCCATACTGAGGTGACAAAGTGAACACAGCAAC 1626
Db 1447 GGCAACAGTTTGTCTATGCTGCTTAACCTCGGGGTGTCAGGCCCGCTGGCCTTC 1506
Qy 1627 TGTGGCGCTCCAGAGCTCTCGAGTGTATCTTGCCCGAGGACCCCGTGTGCGCTGG 1686
Db 1507 TGTGGGAAGCACGCACTCGGAGGACTGTGCTGCGCGGGAGCCCTACTGCGCCTGG 1566
Qy 1687 AGCTTCGGGCTTGTATGTTGTGGGCC 1714
Db 1567 AGCCCGCCACAGCGACCTCGCTGGCTC 1594

RESULT 9

PCT-US02-36071A-167
; Sequence 167, Application PC/TUS0236071A
; GENERAL INFORMATION:
; APPLICANT: Sagres Discovery
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000142
; CURRENT APPLICATION NUMBER: PCT/US02/36071A
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 167
; LENGTH: 4157
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-36071A-167

Query Match 5.4%; Score 215.2; DB 1; Length 4157;
Best Local Similarity 48.9%; Pred. No. 3.3e-47;
Matches 747; Conservative 0; Mismatches 748; Indels 33; Gaps 5;
Qy 211 CCAGAACCTCGCTGCCCATCTCCGAGGCTGACTCTCTATCTCACCCTGTTTGAGCGCTCT 270
Db 163 CCATACCCCGGATCACTCGGGAGCACAGAGAGGTGCACCTGGTGTGAGTTTTCATGAGCCA 222
Qy 271 CATACGTACAAATTAATCTGCTCTCCCTTGTGATCCCTCCCTCCACACACTTTAGTCGGT 330
Db 223 GACATCTACAACTACTCAGCCTTGTGCTGCTGAGGAGGAGGAGACACTTGTATAGAGT 282
Qy 331 GCACGGGATAGCATCTTCGCTTTAAACCTCCCTCTCTCTGGGAAAGACCCCGAAGATC 390
Db 283 GCCGGGAGCGGCTCTCGCTGTGAAGCACTCAACATCTCCGAGAGAGCAGCATGAGTG 342
Qy 391 GACTGATGTGACTGAGACTCAGACAGAACTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGG 447
Db 343 TATTGGAAGGTCTCAGAAGACAAAAGCAAAATGTGCAGAAAGGGGAAATCAAAACAG 402
Qy 448 GACGAATGTCACAATTTTATCCAGATTCTCGCATTTGTCGCTCAATGCTCTCACTCTCCACG 507
Db 403 ACAGAGTCCCTCAACTACATCCGGGTCTCAGCCACTCAGGCCACTTCCCTTTAGTG 462
Qy 508 TCGCGCACCTTCGCTTTTGTATCCGAAGTGCAGGTTTATGATGTGCTCAGTTTCCAGCAG 567
Db 463 TGTGGGACCAACGATCTCCAGCGGCTGTGACCACTGAACCTTAACATCTCTTTAAGTTT 522
Qy 568 GTTGAAGACTTTCAGAGCGCGCGGGGAAATGTCTTTTTCAGCCAGCTCAACGGTACGA 627
Db 523 CTGGGGAATAAAGATGGCAAGGAAAGTGTCTTTCACCCAGCACACAGCATACACA 582
Qy 628 GCTGTATGTGCTGGGCGCTCTACACCGCACTGTGAAGAACTTCTTGGGAGCTGAG 687
Db 583 TCCGTATGTTGATGGAACATTTATTCGGGAGCTGCTATATTTTGGGAAAGTGA 642
Qy 688 CCATATCTCCGAGCTGTGGTTCGAGCTGAGAGCTGATTCGAACAGAGACTTGTCA 747
Db 643 CCATATCTCCGAAATTTCTCCACAGTCTCTGAGGACAGAAATGAATTC----- 697
Qy 748 TCTGGCTTAATGCTCCAGCTTTGTGCAAGTATGCTGCTGAGCCAGCTGAGTGGGG 807
Db 698 -CTGGGTGAACGAGCTAGTTTCTGCTGATGATCGGAAAGCCAGCTCAGCTGCTCCCG 756
Qy 808 GATGAAGATGGAGACGATGAATCTTTTCTTTCACGGAGCTCCCGAGTGTGGAC 867
Db 757 CCGACGCGCAGATGACAGGCTACTTCTTTCAGGAGGTGCTGTGGAGTATGAG 816
Qy 868 TCCTATGAGCGCATCAAGTCCCAAGAGTGGCCGAGTGTGCGGGGAGCTTGGGGG 927
Db 817 TTTGTGTACAGGTGCTGATCCCGGATAGCAAGAGTGTCAAGGGGAGCCAGCGGCGG 876
Qy 928 AGGAAGACCTTCAGCAGAGATGACACGCTTTCTGAAGCTGACCTGCTGCTGCCAGG 987
Db 877 CTGAGGACCTTGCAGAAAGAAATGGACCTCTTCTGAAAGCCCGAGCTCATCTGCTCCCG 936
Qy 988 CCGAGCATGCGCGGCTCCGGGTTCTCAGGCTATGGCAGACTTTCGGCTCAGCTC 1047
Db 937 CCAGACAGCGCTTGGTCTTCAATGCTCGGGGATGCTTCTGCTCAGCTCAGCTC 993
Qy 1048 GGAGCGGAAACCCCATCTTTTATGGATCTTTTCTCCAGATGGGAGGAGCTGCGCATC 1107
Db 994 GGCTGAAGGTGCGCTGTGCTATGCACTTTCACCCACAGCTGAACAAGTGGGCTG 1053
Qy 1108 TCTGCTGTGTGCC-----TTCCGACCCCAAGACATCCGGGAGTGTCTCAATGGT 1158
Db 1054 TCGGAGTGTGCGCTTACAACCTGTCCACAGCGGAGGAGTCTTCTCCCGAGGAGTAC 1113
Qy 1159 CCCTTTAGAGAGCTAAACATGACTGCAACAGGGGAGTGTCTGCTGAGCAACAGAGTG 1218
Db 1114 ATGAGAGACCAACAGTGGAGCAGTCCACACCAAGTGGGTGGCTATATATGGCCCGTA 1173
Qy 1219 CCCCAGCCAGACTGGAGAGTGCATCGCCAAACAATGAAGCTCCAGAGTGTGGATCC 1278

Db	1174	CCCAAGCCGGGCTGGAGGCTGATGCAGAGGAGCGACGGCCGCAACTACACGAGC	1233
Qy	1279	TCACCTCTCCCTGGCAGACCGCGTCTCACCTTTATCAGAGACCAACCCCTCTCATGTGCACAGG	1338
Db	1234	TCCTTGAAATTTGCCAGACAAGCGCTGCAGTTCGTTAAAGACCAACCCCTTTGATGGATGAC	1293
Qy	1339	CCCGTGTTCCGGCTGACGCCCGCCGCCCTCTCGTCTACTACAGATACAGCCTATCTCAGA	1398
Db	1294	TCGGTAACCCCAATAGACAACAGGCCCGAGGTTAATCAAGAAGATGTGAACCTACACCCAG	1353
Qy	1399	GTGGTGGCCCAAGGGTGACCAAGCCTCTCAGGGAAGAATATCAGGTGCTCTACCTGGGG	1458
Db	1354	ATCGTGGTGGACCGGACCCAGGCCCTGGATGGGACTGCTATGATGTCATGTTGTGCAGC	1413
Qy	1459	ACAGAGGATGGACACCTCCACCGGGTGTGGCGATTGGAGCTCAGGCTCAGTGTCTTGGAG	1518
Db	1414	ACAGACGGGGAGCTCTGCACAAGCCATCAGCCTCGAGGCACGCTGTTACATCATCTCGAG	1473
Qy	1519	GATCTGCGCTTTGTTCCAGAACACACGCGGTTGAGAGCATGAATTTGTA-----	1568
Db	1474	GAGACCCAGCTCTTCCAGGACTTTGAGCCAGTCCAGACCCCTGCTGTCTTCAAAGAAG	1533
Qy	1569	--CCAGATTTGGCTCTCTGGTGGGCTCCCATACTGAGGTGACACAAGTGAACACCAAC	1626
Db	1534	GGCAACAGGTTTGTCATATGCTGGCTCTAACTCGGGCGTGTCCAGGCCCCCGCTGGCCCTTC	1593
Qy	1627	TGTGGCCGCTCTCCAGAGCTGCTCGGAGTGATCTTGCCCCAGGACCCCGTGTGCGCTGG	1686
Db	1594	TGTGGGAAGCACGGCACTCTCGAGGACTGTGCTGGCGGGGACCCCTACTGGCGCTGG	1653
Qy	1687	AGCTTCGGGCTTGATGCTTGTTGTGGCCC	1714
Db	1654	AGCCCGCCACAGCGACTCTCGTGGGTC	1681

RESULT 10

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PCT-US02-36071A-165
; Sequence 165, Application PC/TUSO236071A
; GENERAL INFORMATION:
; APPLICANT: Sagres Discovery
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000142
; CURRENT APPLICATION NUMBER: PCT/US02/36071A
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 165
; LENGTH: 2586
; TYPE: DNA
; ORGANISM: Mus musculus
PCT-US02-36071A-165

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	Query Match	5.1%;	Score 205.6;	DB 1;	Length 2586;
	Best Local Similarity	49.2%;	Pred. No. 9.4e-45;		
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QY	309	CTCCCCACACTTTTACGTCGTGCACGGGATAGCATCTTCGCTTTAAACCCCTCCCTTCTC	368		
Db	174	CAAAAGACACTCTGTATCTAGCGCCCGGGAAGCAGTCTTTGCAC	233		
QY	369	TGGGGAAGACCCCGAAGATCGACTGGATGGTACTAGACTCACAGACAGAACTGCAG	428		
Db	234	CTCTGAGAAGCAACATCAGGTATATTGGAGGTCCTGAAGACAAAAAATCCAAGTGTGC	293		

QY	429	GAAGAAAGGCAA----	GAAGAGGAGCAGAAATGTCACAATTTTATCCAGATTCTTCGCCATGTG	485
DB	294	AGAGAGGGGAAATCA	AAGCAGAGCGGAATGCTAAACTACATTCGAGTACTACAGCCACT	353
QY	486	CAATGCCTCTCACCTCCT	CAGTCGCGCACTTCGCTTTGATCCGAAGTCCGGGGTTAT	545
DB	354	AAGCAGACATTTCCCTCT	ATATGTGTGGGACCAATGCGTTCAGGCCACCTGTGACCACCT	413
QY	546	TGATGTGTCCAGT	TTCCAGCAGGTGTGAAGACTTGAGAGCGCGGGGGGAAATGTCTCTTT	605
DB	414	GAACCTTGACATCTTCA	ANGTTCTGGGGAAGAGTGAAGATGGCNAAGAGATGCCCTT	473
QY	606	TGAGCCAGCTCAACGGT	CAGACGTGTAATGGTGGGGCGTCTCTPACACGCCACTGT	665
DB	474	CGACCCCGCCACAGCT	ACACATCAGTCATGTTGGGGCGAGCTCTACTCTGGGAGTC	533
QY	566	GAAGAACCTTCTGGG	ACTGAGCCCATCTCCCGAGCTGTGGTGCAGCTGAGGACTG	725
DB	534	CTATAATTTCTTGG	CGAGTGAACCCATCATCTCTCGAAACTCTTCCACAGTCCCTTGAG	593
QY	726	GATTCGAACAGACAC	CTTGTCCTGGCTTAATGCTCCAGCCCTTTCTCGCAGCATGTGT	785
DB	594	G-----ACGAG	TATGCCATCCGTCGCTGACGAGCCTAGCTTCGTCTTCTGCTGACGT	647
QY	786	CCTGAGCCCCAGCT	GAGTGGGGGATGAAGATGGAGACGATGAAATCTTTTTTCTTCTAC	845
DB	648	GATCCAGAAAGCC	CAGATGTCGCGAGGGTGAAGATGACAAGCTCTACTCTTTTATAC	707
QY	846	GGAGACCTCCGAGT	GTGACTCTATGAGCGCATCAAGGTCCCAAGAGTGGCCCGAGT	905
DB	708	GGAGGTATCCGT	TGGAGTACGAATTCGTCTTCAAGTTGATGATCCCGGAGTTCGCCAGGT	767
QY	906	GTGTGCGGGGACCT	TGGGGCAGAGACCCCTTCAGCAGAGATGGACGACGTTCCTGAA	965
DB	768	GTGCAAGGGCCAC	CAGCGGCTTCGCGACTTGCACAAAAAGTGGACCTCTCTCTTAA	827
QY	966	GGCTGACCTGCTGT	GCCAGGGCCGAGCATGGCGGGCTCCGGGGTCTCGACGCTAT	1025
DB	828	GGCCAGGCTGATCT	GCCTCCAAGCCAGACAGTGGGCTTGCTTCAACATACTTCAGGATGT	887
QY	1026	GGCAGAGTTCCGG	CTCAGCCTGGAGCGGGAACCCCATCTTTTATGGGATCTTTTCCCTC	1085
DB	888	GTTTGTCTGAGG	CG-----CCCGGCTTCAAGGAGCCTGTGTCTATGCGGTCTTCACCC	944
QY	1086	CCAGTGGAGGAGCT	GCATCTCTGCTGTGTGTCCTCCGACCCCAAGACATCTCGGG	1145
DB	945	ACACTGAACAN	TGTGGTCTGTACAGGGTGTGGGCTACACACTGCCACGGTGGAGC	1004
QY	1146	AGT-----GCT	GAATGGTCCCTTTAGAGAGCTAAA--ACATGACTGCAACAGGGGACT	1196
DB	1005	AGTCTTCTCCGT	TGGAAGTACATGCAGAGTGCCACAGTGGAGCAGTCTCACACCAAGT	1064
QY	1197	GCCTGTCTATGG	ACAACAGGTGCCCCAGCCAGCCTGGAGAGTGCATCGCCCAACAT	1256
DB	1065	GGTCGCTTACA	ATGGCCAGTGGCCACTCCCGCAGCTGGAGCGGTATCGACAGTGA	1124
QY	1257	GAAGCTCCAGC	AGTTTGGATCTCTTCCCTGSCACAGCGGTGCTCACTTCTATTCAG	1316
DB	1125	CCGGGAGCCNA	CTTACACAGCTCTTGAATCTCCAGACAAAACACTGCAGTTTGTAA	1184
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QY	1377	TACAGATACAG	CTTATCTAGTCTGTGGGCCACAGGGTGCACAGCTCTCAGGGAAGA	1436
DB	1245	AAAAAGATGTA	AACTTACACCCAGATAGTGGTAGACAGGACCCAGGCCCTGGATGGGACT	1304
QY	1437	ATATGAGCTGT	CTACTCCGGGACAGAGATGACACTTCCACGGGCTCTGCGCATTTGG	1496
DB	1305	CTACGAGCTCA	NTTCAATACACAGCACAGCCGGGAGCTCTGCATAAAGCAGCTCATCTTAC	1364
QY	1497	AGCTCAGCT	CAGTGTCTTGGAGGATCTGGCCTTTGTTCCAGAAACACAGCCGGTGTGAGAG	1556

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 1678620 seqs, 1244745471 residues

Total number of hits satisfying chosen parameters: 3357240

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1673.6	41.8	2893	11	US-09-808-665A-1
2	1673.6	41.8	2894	11	US-09-808-665A-3
3	654	16.3	799	11	US-09-808-665A-5
4	597.8	14.9	928	14	US-10-188-246-13
5	527.4	13.2	777	14	US-10-188-246-15
6	251.8	6.3	3293	14	US-10-149-819-25
7	248.6	6.2	2155	13	US-10-003-152-11
8	248.6	6.2	2155	14	US-10-002-050-11
9	248.6	6.2	2155	14	US-10-002-304-11
10	248.6	6.2	2156	13	US-10-003-152-21
11	248.6	6.2	2156	14	US-10-002-050-21
12	248.6	6.2	2156	14	US-10-002-304-21
13	248.6	6.2	2284	13	US-10-003-152-13
14	248.6	6.2	2284	14	US-10-002-050-13
15	248.6	6.2	2284	14	US-10-002-304-13
16	247	6.2	3781	11	US-09-946-374-252

17	247	6.2	3781	12	US-10-015-387A-252	Sequence 252, App
18	247	6.2	3781	12	US-10-006-130A-252	Sequence 252, App
19	247	6.2	3781	12	US-10-199-672-453	Sequence 453, App
20	247	6.2	3781	12	US-10-241-220-1	Sequence 1, Appli
21	247	6.2	3781	12	US-10-006-172A-252	Sequence 252, App
22	247	6.2	3781	12	US-10-187-749-453	Sequence 453, App
23	247	6.2	3781	12	US-10-194-457-453	Sequence 453, App
24	247	6.2	3781	12	US-10-184-642-453	Sequence 453, App
25	247	6.2	3781	12	US-10-196-747-453	Sequence 453, App
26	247	6.2	3781	12	US-10-015-392A-252	Sequence 252, App
27	247	6.2	3781	12	US-10-017-253A-252	Sequence 252, App
28	247	6.2	3781	12	US-10-173-689-453	Sequence 453, App
29	247	6.2	3781	12	US-10-173-690-453	Sequence 453, App
30	247	6.2	3781	12	US-10-173-691-453	Sequence 453, App
31	247	6.2	3781	12	US-10-173-692-453	Sequence 453, App
32	247	6.2	3781	12	US-10-173-694-453	Sequence 453, App
33	247	6.2	3781	12	US-10-173-698-453	Sequence 453, App
34	247	6.2	3781	12	US-10-173-699-453	Sequence 453, App
35	247	6.2	3781	12	US-10-173-707-453	Sequence 453, App
36	247	6.2	3781	12	US-10-174-569-453	Sequence 453, App
37	247	6.2	3781	12	US-10-174-583-453	Sequence 453, App
38	247	6.2	3781	12	US-10-174-587-453	Sequence 453, App
39	247	6.2	3781	12	US-10-174-589-453	Sequence 453, App
40	247	6.2	3781	12	US-10-174-591-453	Sequence 453, App
41	247	6.2	3781	12	US-10-175-736-453	Sequence 453, App
42	247	6.2	3781	12	US-10-175-742-453	Sequence 453, App
43	247	6.2	3781	12	US-10-175-744-453	Sequence 453, App
44	247	6.2	3781	12	US-10-175-745-453	Sequence 453, App
45	247	6.2	3781	12	US-10-175-748-453	Sequence 453, App

ALIGNMENTS

RESULT 1

- US-09-808-665A-1
- Sequence 1, Application US/09808665A
- Publication No. US2003002282A1
- GENERAL INFORMATION:
- APPLICANT: David Michalovich
- APPLICANT: Trudy Rachel Doe
- APPLICANT: Phillip David Hayes
- TITLE OF INVENTION: NOVEL COMPOUNDS
- FILE REFERENCE: GP-30036-C1
- CURRENT APPLICATION NUMBER: US/09/808.665A
- CURRENT FILING DATE: 2001-03-15
- PRIOR APPLICATION NUMBER: 09/160,762
- PRIOR FILING DATE: 1998-09-24
- PRIOR APPLICATION NUMBER: 98300693.3
- PRIOR FILING DATE: 1998-01-30
- PRIOR APPLICATION NUMBER: 9816423.9
- PRIOR FILING DATE: 1998-07-28
- PRIOR APPLICATION NUMBER: 9816676.2
- PRIOR FILING DATE: 1998-07-30
- NUMBER OF SEQ ID NOS: 6
- SOFTWARE: FastSeq for Windows Version 3.0
- SEQ ID NO 1
- LENGTH: 2893
- TYPE: DNA
- ORGANISM: HOMO SAPIENS

US-09-808-665A-1

Query Match	41.8%	Score 1673.6;	DB 11;	Length 2893;
Best Local Similarity	82.2%	Pred. No. 0;		
Matches 2012;	Conservative	0;	Mismatches 319;	Indels 117; Gaps 3;
Qy	1	GCCGAGCCCGCAGTAGCGGTACTAAGTAGAGGTGCTGGAGCGCGCCACCCCGGCAC	60	
Db	35	GCCGAGCCAGTAGTCCCGCGCGCTTGCAGAGAGCGTAGCTTGCAGCGCCACCCCGGC	94	
Qy	61	CAGCGGAGCCAGAGATGCTTGCAGGCGCGCCCGCGCGCGCGCGCGCGCGCT	120	
Db	95	CAGCGGAGCCAAAGATGCCGCGCTCTGCTGCGCGCGCGCGCGCGCGCGCT	154	


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Db 2198 CTGGCCAAAGAGGGCAGTGGGTTTTGGTGGATTCTCACCACCTTCTCCTGCTTGATCTTGC 2257
Qy 2341 CCAAGCCAGCCACATCCGCTCACTGGGGGCTCTAGCCACGCTGTGATGAGACCTCC 2400
Db 2258 CCAAGCCAGCCACATCCGCTCACTGGGGCTCTCTAGCCACATGTGATGAACATCC 2317
Qy 2401 ATCTAAAGCCGGGAAATAGCTGCCAGCCATGAGCAGCTCTCTGGAAC 2448
Db 2318 ATCTAGAGCTGGCAATGACCACCTAGTGTATAGTGATCACTGGAAC 2365

RESULT 2
US-09-808-665A-3
; Sequence 3, Application US/09808665A
; Publication No. US20030022822A1
; GENERAL INFORMATION:
; APPLICANT: David Michalovich
; APPLICANT: Trudy Rachel Doe
; APPLICANT: Philip David Hayes
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30036-C1
; CURRENT APPLICATION NUMBER: US/09/808,665A
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/160,762
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 98300693.3
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 9816423.9
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 9816676.2
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2894
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-808-665A-3

Query Match 41.8%; Score 1673.6; DB 11; Length 2894;
Best Local Similarity 82.2%; Pred. No. 0;
Matches 2012; Conservative 0; Mismatches 319; Indels 117; Gaps 3;

Qy 1 GCCAGGCGCCGCGAGTAGTACGCGTACTAGTAGAGGCTGCTGAGCGCGCCGCCACCCGGCAC 60
Db 35 GCCAGGCGCCAGTAGCCCGGGCCCTGAGAGAGCCGTAGTTGCGCGCGCACCCGGCGC 94
Qy 61 CAGGCGGAGCAGAGATGCTTGGCCAGGCGCGAGCGGCCCGCGCGGGGCCCGCGCGCCT 120
Db 95 CAGGCGGAGCAAGATGCGGCGCTCTGCTGGCGGCCCGCGCGGGTCCCGGGCAGCCT 154
Qy 121 CCGGTCTTCCCTCCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 155 ACAGCCTCGCCCTTCCC-----GCTACTGCTGCTGGCGGTGCTGAGCGGC 199
Qy 181 CCGGTGTCGCGCGCGCTCCCGCTCAGTGCCAGAACCTCGCTGCCATCTCCGAGGCT 240
Db 200 CCGGTATCCGCGCGGTCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 259
Qy 241 GACTCTCTATCACCCTGTTGACGCGTCTCATAGTACAAATTAATCTGCTCTCTCTG 300
Db 260 GACTCTCTATCACCCTGTTGACGCGTCTCATAGTACAAATTAATCTGCTCTCTCTG 319
Qy 301 GATCCTGCTCCACACATTTTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 320 GATCCTGCTCCACACATTTTATGTTGGCGCGCGGACACCATCTTCGCTTTTATCCCTG 379
Qy 361 CCCTTCTCTGGGAAAGACCCGAGGATGACCTGAGTGGTACCTTGAGACTCAGACAG 420
Db 380 CCCTTCTCAGGGGAGAGACCCCGAGGATGACTGGATGGTTCCTTGAGGCTCAGACAG 439
Qy 421 AACTGCAGGAAGAGCAAGAAAGAGACGAATGTCACAATTTTATCCAGATTCTCGCC 480
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Db 440 AACTGTAGGAAGAAAGCAAGAAAG----- 466
Qy 481 ATTGTCAATGCTCTCACCTCCTCAGCTGCGGCACCTTCGCTTTTGTATCCGAAGTGGCGG 540
Db 467 -----GATGTGTCAGGTTCCAGAGCTTGAAGACTTGAGATGGCGGGGAAATGT 466
Qy 541 GTTATTGATGTCCAGTTTCCAGCAGGTTGAAAGACTTGAGAGCGGCGCGGGGAAATGT 600
Db 467 -----GATGTGTCAGGTTCCAGAGCTTGAAGACTTGAGATGGCGGGGAAATGT 520
Qy 601 CCTTTTGAGCAGCTCAACGGTTCAGCAGCTCTAATGCTGGGGGCGTCTCTTACACCGCC 660
Db 521 CCTTTTGAGCAGCTCAGCGTTCAGCAGCTCTAATGCTGGGGGCGTCTCTATGCTGCC 580
Qy 661 ACTGTGAAGAACTCTCTGGGACTGAGCCCATCATCTCCGAGCTGTGGGTGGCGAGT 720
Db 581 ACTGTGAAGAACTACCTGGGACGAGCCAAATATCACAGAGAGTGGGTGCTGCCGAG 640
Qy 721 GACTGGATTGGAACAGAGACCTTGTATCTCTGGCTTAATGCTCCAGCCTTTGTTCAGCT 780
Db 641 GACTGGATTGGAACAGATACCTTGCCTTCCTGGCTGAACGCCGCCAGCCTTTGTCCGAGCC 700
Qy 781 ATGTCTCTGAGCCAGCTGAGTGGGGGATGAAGATGAGAGATGAATCTTTTTC 840
Db 701 GTGGCCTTGAGCCAGCCGAATGGGGGATGAAGATGAGAGACGAGAAATCTACTTCTTC 760
Qy 841 TTCAGGAGACTCCCGAGTGTGGACTCTTATGAGCCCATCAAGTCCCAAGAGTGGCC 900
Db 761 TTTACGGAGACTTCCCGAGCTTTGACTATACGAGCCCATTAAGTCCCAAGTGGCC 820
Qy 901 CGAGTGTGTGGGGGACCTTTGGGGGAGAGACCTTTACAGCAGATGAGCAGACGTTT 960
Db 821 CGTGTGTGTGGGGGACCTCGGGGGCGGAGACCTTCAGCAGAGATGAGCAGACGTTT 880
Qy 961 CTGAAGCTGACCTGCTGTGCCAGGCGCCGAGCATGGCCGGGCTTCGCGGTTCCTGAG 1020
Db 881 TTGAAGCTGACCTGCTGTGCCAGGCGCTGAGCATGGCCGGGCTTCAGCAGTGTCTGCGAG 940
Qy 1021 GCTATGCGAGACTTCGGCCTCAGCCTGGAGGGGAACCCCATCTTTATGGGATCTTT 1080
Db 941 GATGTGTGCTGCTGCTGACCTGAGCTTGGGCGAGGACTCCCATCTTTTATGGCATCTT 1000
Qy 1081 TCTCTCCAGTGGGAGAGCTGCCATCTCTGCTGTGTGCTTCCGACCCCAAGACATC 1140
Db 1001 TCTTCCAGTGGGAGGCGCTACTATCTCTGCTGTGCTTCCGACCAACACAT 1060
Qy 1141 CGGCGAGTGTGAATGTCTCTTTAGAGAGCTAAACATGACTGCAACAGGGAGTGCCT 1200
Db 1061 CGGACAGTGTGAATGTCTCTTTCAGAGAACTAAACATGACTGCAACAGAGGAGTGCCT 1120
Qy 1201 GTCATGGACACAGAGGTGCGCCAGCCAGCTGGAGAGTGCATCGCCCAACAAATGAAG 1260
Db 1121 GTCGTGGACAATGATGTGCCCCAGCCAGAGCTGGAGAGTGCATCACCAACAAATGAAG 1180
Qy 1261 CTCAGCAGATTTGGATCTCTACTCTCCCTGCCAGACCGCTGCTCACCTTTATCAGAGAC 1320
Db 1181 CTCGCGCACTTTGGCTCATCTCTCTCTGCTGACCGCGTACTCACCTTCATCCGGGAC 1240
Qy 1321 CACCTCTCATGAGACAGCGCTGTTCGCGCTGACGGCGCGCCCTGCTGCTGCTACTACA 1380
Db 1241 CACCCACTCATGAGACAGCGCAGTGTTCAGCTGATGGCCACCCCTCTGCTGCTACTACA 1300
Qy 1381 GATACAGCTATCTCAGAGTGTGCGCCACAGGGTGACACGCTCTCAGGGAAAGAAATAT 1440
Db 1301 GATACAGCTATCTCAGAGTGTGCGCCACAGGGTGACACGCTCTCAGGGAAAGAGATAT 1360
Qy 1441 GAGCTGCTTACTCTGGGAGACAGAGATGACACCTTCCACCGGGTGTGCGGATTTGAGCT 1500
Db 1361 GATGTCTTACTCTGGGAGACAGAGATGACACCTTCCACCGAGAGTGTGCGGATCGGAGCT 1420
Qy 1501 CAGCTCAGTGTCTGGAGGATCTGGCCTTGTTCAGAGAACACACAGCCGTTGAGAGCATG 1560
Db 1420 CAGCTCAGTGTCTGGAGGATCTGGCCTTGTTCAGAGAACACACAGCCGTTGAGAGCATG 1560
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Db 1421 CAGCTCAGCGTCTTGAAGATCTGGCCCTTATTCACAGAGCCAGCCAGCTTGAGAACATG 1480
QY 1561 AAATTGTACACAGATTGGTCTCTGGTGGGTCCCATCTAGGTGACACAAAGTGAACACC 1620
Db 1481 AATTTTACACAGCTGGTCTCTGGTGGTGGTCCCGTACTGAGGTGACACAAAGTGAATACA 1540
QY 1621 AGCAACTGTGGCGGTCTCAGAGCTCTCGGAGTGTATCTGGCCAGGACCCCGGTGTC 1680
Db 1541 ACCAAGTGTGGCGGTCTCAGAGCTCTCAGAGTGTATCTGGCCAGGACCCAGTCTGT 1600
QY 1681 GCTTGAGGTCTCGCGGTCTGATGCTGTGTGGCCAGCGCGGAGCACCGCGGATGGTT 1740
Db 1601 GCTTGAGGTCTCGCGGTCTGATGATGTGTGGCCATGCCGGGAGCACCGAGGTGGTC 1660
QY 1741 CAAGATATAGAGTACAGGATGTCTCTTTGTCCAAAGAACTGGAGAACATCC 1800
Db 1661 CAAGACATAGAGTACAGAGTGTCTCTCTTTGTCTTAAGAGCTTGAGAACGTCCA 1720
QY 1801 GTAGTGTGAAGTTCGGTGGTCTACTGTGGCCAGCTGGTCTGCCATGTTCCCGCACT 1860
Db 1721 GTAGTGTGAAGTTCGGTGGTCTACTGTGGCCAGCTGGTCTGGCATGTCTTCCAAGC 1780
QY 1861 TCTGCTGGGCATCTGTGTGGCCAGCCAGCCAGTGGAGTGAAGTCTGCTCACTCCCGG 1920
Db 1781 TCAGCATGGCATCTCTGTGTGGCCAGCCAGCCAGTGGAGTGAAGTCTGCTCACTCA 1840
QY 1921 AGGATGGACTAGAGTGTGTGTGACCCAGGGCCATGGGGCTTATGCTTCCAGTGT 1980
Db 1841 CGGATGGACTGGAGTGTGTGTGACCCAGGGCCATGGGGCTTATGCTTGAATCT 1900
QY 1981 CAGGAGGTGGAGCCCGCGTGTGGTGTGTGATAGTGTGGTGGGAGCCAGCGG 2040
Db 1901 CAGGAGGTGGGAGCCCGCGTGTGTGATAGTGTGGTGGGAGCCAGCGG 1960
QY 2041 GGACCTCAAAACCGGGCCACACCGTGTGGGGGTGGATGTTGGCTTTCTCCTGGGT 2100
Db 1961 GATGCTCCGAGCGGGGCCACAC--AGTGGGGGGGAGTGGTGGCTTTCTTCTGGGG 2017
QY 2101 GTTCTTGACATCCCTCACTCTCTCTCTGATTGGTGGCGGTGAGTGGTGGTGGTGGT 2160
Db 2018 ATTCTCGCAGCATCCCTGACTCTCATCTGATTGGTGGCGGTGAGTGGGAGCCAG 2077
QY 2161 AGGAGCTTCTAGTAGACAAAGTGGGCTTAGATCTGGGGCTCCACCTTCTGGGACC 2220
Db 2078 AGGAACTTCTGGCTAGACAAAGTGGGCTTGGACCTGGGGGCTCCACCTTCTGGGACC 2137
QY 2221 ACAAGCTATAGTCAGGACCTCCCTCTCTCTCGCTGAAGATGAAGGCTGCCCTGGCC 2280
Db 2138 ACNAGCTACAGCAAGACCTCCCTCCCTCTCTCTGAAGATGAGCGGTGGCGTGGCC 2197
QY 2281 CTGGGTAAGCGGGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2340
Db 2198 CTGGGCAAGAGGGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2257
QY 2341 CCNAGCCAGCCACATCCGGCTCACTGGGGGCGCTTACGCCAGCTGTGATGAGACCTCC 2400
Db 2258 CCNAGCCAGCCACATCCGGCTCACTGGGGGCGCTTCTTACGCCAGCTGTGATGAAACATCC 2317
QY 2401 ATCTAAGCCGGGAAATGACTGCCAGCATGAGCAGTCTCTGGAAC 2448
Db 2318 ATCTAGAGCTGGGCAATGACCACTAGTGTATAAGTATGATCTGGAAC 2365
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RESULT 3
US-09-808-665A-5
; Sequence 5, Application us/09080665A
; Publication No. US2003002282A1
; GENERAL INFORMATION:
; APPLICANT: David Michaelovich
; APPLICANT: Trudy Rachel Doe
; APPLICANT: Philip David Hayes
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30036-CL

```
; CURRENT APPLICATION NUMBER: US/09/808,665A  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: 09/160,762  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 98300693.3  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 9816423.9  
; PRIOR FILING DATE: 1998-07-28  
; PRIOR APPLICATION NUMBER: 9816676.2  
; PRIOR FILING DATE: 1998-07-30  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 799  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (720)  
; OTHER INFORMATION: OTHER INFORMATION: Partial EST derived sequence  
US-09-808-665A-5  
  
Query Match 16.3%; Score 654; DB 11; Length 799;  
Best Local Similarity 88.6%; Pred. No. 2e-170;  
Matches 708; Conservative 0; Mismatches 91; Indels 0; Gaps 0;  
  
QY 1126 CGACCCCAAGACATCCGGCAGTGTGATGTGTCCTTTAGAGAGCTAAACATGACTGC 1185  
Db 1 CGACCACACAGATTCGGACAGTGTGATGTGTCCTTCAGAGACTAAACATGACTGC 60  
  
QY 1186 AACAGGGGACTGCCTGTCTATGGACACGAGGTGCCCCAGCCAGACCTGGAGAGTGCATC 1245  
Db 61 AACAGAGGACTGCCTGTCTGTGGACATGATGTGCCAGCCAGACCTGGAGAGTGCATC 120  
  
QY 1246 GCCAACACATCAAGCTCCAGCAGTGTGATCTCTCACTCTCCCTGCCACACCGCTGCTC 1305  
Db 121 ACCAACACATGAAGCTCCGGCAGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180  
  
QY 1306 ACCTTTATCAGAGACACACCTCTCTATGGACAGCGCGTGTCCCGGCTGACGCGCCGCC 1365  
Db 181 ACCTTCATCCGGACACACCTCTCTATGGACAGCGCGTGTTCCTCAGCTGATGGCCACCC 240  
  
QY 1366 CTGCTGGTCACTACAGATACAGCTATCTCAGAGTGTGGCCACAGGCTGACCGCTTC 1425  
Db 241 CTGCTGGTCACTACAGTTCACAGCTATCTCAGAGTGTGGCCACAGGCTGACCGCTTC 300  
  
QY 1426 TCAGGAAAGATATGACGTCTCTACCTGGGACAGAGATGGACACCTCCACCGGCT 1485  
Db 301 TCAGGAAAGATATGATGTCTCTACCTGGGACAGAGATGGACACCTCCACCGGCA 360  
  
QY 1486 GTGCGCATTTGAGCTCAGCTCAGTGTCTTTGGAGGATCTGGCTTGTTCAGAACACACAG 1545  
Db 361 GTGCGGATCGGAGCTCAGCTCAGCTCAGCTTCTTGAAGATCTGCGCTTATTCAGAGCCACAG 420  
  
QY 1546 CCGGTTGAGAGCATGAAATTTACACGATTTGGCTCTCTGGTGGGTGCCATCTAGAGTG 1605  
Db 421 CCAGTTGAGAACATGAAATTTACACAGTGGCTCTCTGGTGGGTGCCATCTAGAGTG 480  
  
QY 1606 ACACAAGTGAACACAGCAACTGTGGCGCTCTCCAGAGTGTCTCGAGTGTATCTCGGCC 1665  
Db 481 ACACAAGTGAACACCAACTGTGGCGCTCTCCAGAGTGTCTCGAGTGTATCTCGGCC 540  
  
QY 1666 CAGGACCCCGTGTGGCGCTTGGAGCTTCCGGCTTGTGTTGTGTGGCCACCGCGGAG 1725  
Db 541 CAGGACCCAGTCTGTGGCTGGAGCTTCCGGCTGGATGAGTGTGGCCATCGCGGGAG 600  
  
QY 1726 CACCGGGGATGGTTCAAGATATAGAGTACAGCGGATGTCTCTTTGTGTCCAAAGAA 1785  
Db 601 CACCGAGGTTGGTCCAAAGACATAGAGTACAGAGTGTCTCTCTTTGTGTCTAGAGAG 660  
  
QY 1786 CCTGGAGAACATCCCGTAGTGTTCAGGTTCCGGTGGCTGTGTGTGTGGCCACCTGGCTG 1845  
Db 661 CCTGGAGAACGTCACAGTAGTGTTCAGGTTCCGGTGGCTGTGTGTGTGGCTGTGTGT 720
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;; PRIOR APPLICATION NUMBER: 60/304502
;; PRIOR FILING DATE: 2001-07-11
;; PRIOR APPLICATION NUMBER: 60/305011
;; PRIOR FILING DATE: 2001-07-12
;; PRIOR APPLICATION NUMBER: 60/306085
;; PRIOR FILING DATE: 2001-07-17
;; PRIOR APPLICATION NUMBER: 60/326981
;; PRIOR FILING DATE: 2001-10-14
;; PRIOR APPLICATION NUMBER: 60/360923
;; PRIOR FILING DATE: 2002-02-28
;; PRIOR APPLICATION NUMBER: 60/363636
;; PRIOR FILING DATE: 2002-03-12
;; PRIOR APPLICATION NUMBER: 60/373063
;; PRIOR FILING DATE: 2002-04-16
;; NUMBER OF SEQ ID NOS: 60
;; SOFTWARE: Custom
;; SEQ ID NO 15
;; LENGTH: 777
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)..(777)
US-10-188-246-15

Query Match 13.2%; Score 527.4; DB 14; Length 777;
Best Local Similarity 90.2%; Pred. No. 2.2e-135;
Matches 564; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
QY 193 CCGCTCCCGCTAGTGGCCAGAACCTCGCTGCCATCTCGAGGCTGACTCTCTATCTC 252
DB 7 CCGCTCCCGCTAGTGGCCAGAACCTCGCTGCCATCTCGAGGCTGACTCTCTATCTC 66
QY 253 ACCCGTTTGGACGCTCATACGTACAACTTCTGCTCTCTCTGATCTCTGCTCTCTG 312
DB 67 ACCCGTTTGGACGCTCATACGTACAACTTCTGCTCTCTCTGATCTCTGCTCTCTG 126
QY 313 CACACACTTACCTCGGTCGACGGGATAGCATCTTTCGCTTTAACCTCTCCCTTCTCTGG 372
DB 127 CACACACTTATGTGGCGCGCGGACACCATCTTTCGCTTTATCTCTCTCTCTCTG 186
QY 373 GAAGACCCCGAAGATCGACTGGATGGTACTGAGACTCAGACAGAACTGCAAGGAG 432
DB 187 GAGACCCCGGAGGATGAGTGGATGGTTCCTGAGGCTCAGACAGAACTGTAGGAG 246
QY 433 AAAGCAAGAAAGAGGAGCAATGTACAACTTTTATCCAGATCTCGCCATCTGCAATGCC 492
DB 247 AAAGCAAGAAAGAGGAGCAATGTACAACTTTTGTCCAGATCTCGCCATCTGCAATGCC 306
QY 493 TCTACCTCTCAGCTCGGCACTTTCGCTTTTGTATCCGAGTGGGGGTTATGATGTG 552
DB 307 TCTACCTCTCAGCTCGGCACTTTCGCTTTTGTATCCGAGTGGGGGTTATGATGTG 366
QY 553 TCCAGTTTCCAGCAGTTGAAGACTTGAGCGCGCGGGGAAATGTCTTTTGAAGCA 612
DB 367 TCCAGTTTCCAGCAGTTGAAGACTTGAGAGTGGCGGGGAAATGTCTTTTGAAGCA 426
QY 613 GCTAACGGTCAGCAGCTGTATGCTGGGGCGTCTCTACACCGCCACTGTGGAAGAC 672
DB 427 GCTACGGTTCAGCAGCTGTATGCTGGGGGTCTCTATGCTGCCACTGTGAAGAC 486
QY 673 TTCCTGGGAGTGAACCCATCATCTCCGAGCTGTGGGTGAGCTGAGAGTGGATTCGA 732
DB 487 TACCTGGGAGTGAACCCATCATCTCCGAGCTGTGGGTGAGCTGAGAGTGGATTCGA 546
QY 733 ACAGAGCTTGTCTATCTGCTTAACTCTCAGCTTGTTCGCAAGCTATGGTCTGAGC 792
DB 547 ACAGATCTTGTCTCTGCTTAACTCTCAGCTTGTTCGCAAGCTATGGTCTGAGC 606
QY 793 CCAGCTGAGTGGGGGATGAAGATG 817
DB 607 CCAGCCGAATGGGGGATGAAGATG 631

RESULT 6

US-10-149-819-25
;; Sequence 25, Application US/10149819
;; Publication No. US20030044913A1
;; GENERAL INFORMATION:
;; APPLICANT: INCYTE GENOMICS, INC.
;; APPLICANT: YUE, Henry
;; APPLICANT: AZIMZAI, Yalda
;; APPLICANT: TANG, Y. Tom
;; APPLICANT: PATTERSON, Chandra
;; APPLICANT: BAUGHN, Mariah R.
;; APPLICANT: LU, Dyung Aina M.
;; APPLICANT: SHAH, Purvi
;; APPLICANT: LAL, Preeti
;; APPLICANT: AU-YOUNG, Janice
;; APPLICANT: BUREFORD, Neil
;; TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
;; FILE REFERENCE: PF-0760 PCT
;; CURRENT APPLICATION NUMBER: US/10/149,819
;; CURRENT FILING DATE: 2002-06-10
;; PRIOR APPLICATION NUMBER: 60/172,852; 60/172,354
;; PRIOR FILING DATE: 1999-12-10; 1999-12-16
;; NUMBER OF SEQ ID NOS: 42
;; SOFTWARE: PERL Program
;; SEQ ID NO 25
;; LENGTH: 3293
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; NAME/KEY: misc_feature
;; OTHER INFORMATION: Incyte ID No. US20030044913A1 1674661CB1
US-10-149-819-25

Query Match 6.3%; Score 251.8; DB 14; Length 3293;
Best Local Similarity 52.3%; Pred. No. 8.6e-59;
Matches 706; Conservative 0; Mismatches 627; Indels 18; Gaps 6;
QY 383 GAAGATCGACTGGATGGTACCTGAGACTCAGACAGACAGAACTGAGGAGAAAGCAAG- 441
DB 387 GAGCATCTCTGGGAGGCCGCCGTGGAGAAAGAACTGAGTGTATCCAGAAGGGAAGA 446
QY 442 --AAAGAGGAGAGTGTACAAATTTTATCCAGATTTCTGCCCATTTGTCAATGCTCTCAC 499
DB 447 ACAACAGACAGAGTGTCAACTTTCATCCGCTTCTCTGAGCCCTTACAACTGCTCCACC 506
QY 500 TCCTCAGCTGGGCACTTCCGCTTTTGATCCGAAGTGGGGTTATGTATGTGTCCAGTT 559
DB 507 TGTACGTCTGTGGCACTTACGCTTCCAGCCCAAGTGCACCTTACGCTCAACATGCTCACCT 566
QY 560 TCCA---GCAGTTTGAAGACTTTGAGAGCGCGCGGGGAAATGTCTTTTGAAGCAGCTC 616
DB 567 TCACTTTGAGCATGAGAGATTTGAAGATGGGAAGGCAAGTGTCTCTATGACCAGCTA 626
QY 617 AACGTCAGAGCTGTATGCTGGGGGCTCTCTACACGCCACTGTGAAGAACTTCC 676
DB 627 AGGCGCATCTGGCCTTCTTGTGGATGGTGAAGTGTACTCGGCCACACTCAACAACCTCC 686
QY 677 TGGGAGCTGAGCCCATCATCTCCCGAGCTGTGGGTGAGCTGAGGAGCTGGATTCGAAGAC 736
DB 687 TGGGAGCCGAGACCCATTTCTGCTTAACATGGGGC---CCACCACTCCATGAAGACAG 743
QY 737 AGACCTTGTCTCTCTGGCTTAAATGCTCCAGCCTTTGTGCGAGCTATGGTCTGAGCCCC 796
DB 744 AGTACTGGCCTTTTGGCTCAACGAACCTCACTTTGTAGGCTCTGCTCTATGATACCTGAGA 803
QY 797 CTGAGTGGGGGATGAAGATGAGACGATGAATTAATTTTCTTCTTCTCAGGAGACTTCC 856
DB 804 CTGTGGGAGCTTACGCGGGGACGACGACAGAGTGTACTTCTTCTTCTCAGGAGCGGGCAC 863
QY 857 GAGTGTGTGACTCTCTATGAGCGCATCAAGGTGCCCCAAGAGTGGCCGAGTGTGTGCGGGG 916
DB 864 TGGAGTCCGACTGCTATCCGAGCAGAGGTGGTGGCTGCTGTGCGCCGCTGTCTCGAAGGGG 923

Db 1193 GCCCTATAAGGAGTACCATGAGGAAGCCAGAGTGGGACCGCTACACTGACCCT---G 1249
Qy 1217 TGCCCCAGCCAGACCTGGAGAGTGCATCCGCCAACACATGAAGCTCCAGCAGTTGGAT 1276
Db 1250 TACCAGCCCTCGCGCTGGCTCTGCATTAAACAACCTGGCATCGGCCACGGCTACACCA 1309
Qy 1277 CCTCACTCTCCCTGCCAGACCGGCTGCTACACCTTTATCAGAGACCAACCTCTCATGGACA 1336
Db 1310 GCTCCCTGGAGCTACCCGCAACATCTCAACTTCGTCAAGAAGCACCCGCTGATGGAGG 1369
Qy 1337 GGCCCGTGTTCGCCGGCTGAGCGGCCCGCCCTGCTGCTCACTACAGATACAGCCCTATCTCA 1396
Db 1370 AGCAGTGGGGCCCTCGGTGGAGCGGCCCTGCTGCTGAGAAGGCGCAACCTTCACCC 1429
Qy 1397 GAGTCGTGGCCCAAGGGTGACAGCCTCTCAGGGAAGAATATAGCTGCTCTACCTGG 1456
Db 1430 ACCTGGTGGCCGACCGGTTACAGGACTTGATGAGCCACCTATACAGTGTCTTTCATTG 1489
Qy 1457 GGACAGAGATGACACCTCCACCGGGCTGTGGGCATTGGAGCTCAGCTCAGTGTCTTGG 1516
Db 1490 GCACAGAGACGGCTGGCTGCTCAAGGCTGTGAGCCTGGGGCCCTGGGTTCACCTGATTG 1549
Qy 1517 AGGATCTGGCCTTGT---CCAGAAACACAGCCGGTTGAGAGCATGAATGTACCAAG 1573
Db 1550 AGGAGTCAGCTGTTTGACAGGAGCCCATGAGAAGCCTGGTCTATCTCAGAGCAAGA 1609
Qy 1574 ATTGGCTCTGGGGCTCCCTACTACTGAGGTGACACAAAGTGAACACCACTGTGGCC 1633
Db 1610 AGCTGCTCTTGGCGGCTCCGCTCTCAGCTGGTGCAGCTGCCCGTGGCGGACTGCATAA 1669
Qy 1634 GTCTCAGAGCTCTCGGAGTGTATCTTGGCCAGGACCGGCTGTGGCGCTGGAGTTCC 1693
Db 1670 AGTATCGCTCTGTGACAGTGTGCTCTCGCCGGAGCCCTATTGCGCTGGAGCGTCA 1729
Qy 1694 GGCTTGATGCTGTGTGGCCACAGCCGGCGGA 1724
Db 1730 ACACAGCCGCTGTGTGGCGGTGGTGCCA 1760

RESULT 8

US-10-002-050-11
; Sequence 11, Application US/10002050
; Publication No. US20030032095A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meijia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: No. US20030032095A1e1 Nucleic Acid Sequences Encoding Human Semaph
; FILE REFERENCE: 15966-554 Cura-54 CON-S14
; CURRENT APPLICATION NUMBER: US/10/002,050
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 2155
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (166)..(1935)
US-10-002-050-11

Query Match 6.2%; Score 248.6; DB 14; Length 2155;
Best Local Similarity 52.1%; Pred. No. 5.4e-58;
Matches 704; Conservative 0; Mismatches 629; Indels 18; Gaps 6;

Qy 383 GAAGGATCGAAGTGGTACCTGAGACTCACAGACAGAACTGCAGGAAGAAAGGCAAG- 441
Db 419 GAGCGATCTCTGGGAGGCCCGTGGAGAAGAAGACTGAGTGTATATCCAGAAAGGAAGA 478
Qy 442 --AAAGAGACAGAAATGTCACAAATTTATCCAGATTTCTCGCCATTTGCAATGCCTCTCACCC 499
Db 479 ACAACAGACACCGAGTCTTCAACTTCATCCGCTTCTGACAGCCCTCAAAATGCCTCCACC 538
Qy 500 TCTCTACGTGGCGACCTTTCGCTTTTATCCGAAGTGGGGGTTATTGATGTCTCCAGTT 559
Db 539 TGTACGTCTGTGGCAGCTAGCCCTCCAGCCCAAGTGCACCTACGTCAACATGCTCACCT 598
Qy 560 TCCA---GCAGGTTGAAAGACTTTGAGAGCGCGGGGAAATGTCCTTTTGGAGCCAGCTC 616
Db 599 TCACTTTGGAGCATGAGAGTTTGAAGATGGGAAGGCAAGTGTCTCTATGACCCAGCTA 658
Qy 617 AACGGTCACAGCTGTAAATGGCTGGGGGGTCTCTACACCGCCCACTGTGAAGAAGCTTCC 676
Db 659 AGGGCCATGCTGGCCCTCTTGTGGATGGTGAAGTGTACTCGGCCACACTCAACAACTTCC 718
Qy 677 TGGGACTGAGCCCATCATCTCCGAGCTGTGGTGCAGCTGAGGACTGGATTTCGAACAG 736
Db 719 TGGGCACGAAACCATTTATCTCGCTAATCATGSGGC---CCACCACTCCATGAACACAG 775
Qy 737 AGACCTTGTCATCTCGCTTAATGTCTCAGCCCTTTGTGCGAGCTATGGTCTCTGAGCCAG 796
Db 776 AGTACCTGGCTTTTGGCTCAACGAACCTCACTTTCTAGGCTCTGCTATGACCTGAGA 835
Qy 797 CTGAGTGGGGGATGAAGATGGAGACGATGAATCTTTTTTTTCTTCAGGAGACCTCCC 856
Db 836 GTGTGGGAGCTTTCAGGGGGAGCAGCAAGGTCTACTTCTTCTTCAGGAGCGGGCAG 895
Qy 857 GAGTGTGAGCTCTTATGAGCGCATCAAGGTCCCAAGAGTGGGCCCGAGTGTGTGCGGGG 916
Db 896 TGGAGTCCACGCTCTATGCCGAGCAGTGGTGGCTGTGTGGCCGCTGTCTGCAAGGGCG 955
Qy 917 ACCTTGGGGGAGAGAACCTTTCAGCAGAGATGGACAGCTTTCTTGAAGGCTGACCTGC 976
Db 956 ATATGGGGGCGCAGGACCTTCGAGAGGAAGTGGACACAGTTCCTTGAAGGCGCGCTGG 1015
Qy 977 TGTGCCAGGGCCGAGCATGGCCGGGCTCTCGAGGCTATGGCAGAGCTTC 1036
Db 1016 CATGCTCTGCCCGAACTGGCAGCTTCTTCAACCACTGCGAGGCGATG---CACACCC 1072
Qy 1037 GGCCTCAGCCTGGAGCGGAACCCCATCTTTTATGGATCTTTTCTCCAGTGGGAAG 1096
Db 1073 TGCAGGACACCTCTCTGGCAACAACACACCTCTTTTGGGGTCTTCAAGCACAGTGGGGTG 1132
Qy 1097 GAGCTGCCATCTCTGCTGTGTGCTTCCGACCCCAAGACATCCGGGCGAGTGTGAATG 1156
Db 1133 ACATGTACCTGTGCGCCATCTGTGATACCACTTGGAGAGATCCAGCGGGTGTGGAGG 1192
Qy 1157 GTCCCTTTAGAGAGCTAAACATGACTGCAACAGGGGACTGCTGTCTATGGACACAGGAG 1216
Db 1193 GCGCCCTAAGAGGTACCATGAGGAAGCCCAAGTGGGACCGCTACACTGACCTC---G 1249
Qy 1217 TGCCCCCAGCCAGACTTGAGAGTGCATCGCCCAACAACATGAAGTCCACAGTGTGGAT 1276
Db 1250 TACCAGCCCTCGGCTGCTCGTAACTAACAACCTGGCATCGGCCACAGGCTACACCA 1309
Qy 1277 CCTCACTCTCTGCGCAGACCGGCTGCTACCTTTATCAGAGACCAACCTCTCATATGGACA 1336
Db 1310 GCTCCCTGGAGCTACCCGCAACATCTCAACTTGTCAAGAAGCAACCGCTGATGGAGG 1369
Qy 1337 GGCCCGTGTTCGGGCTGACGGCCGCCCCCTCTGCTACTACAGATACAGAGCTTATCTCA 1396
Db 1370 AGCAGTGGGGCTCGGTGGAGCCGCCCCCTCTGCTGAAGAAGGCGCAACCTTCACCC 1429
Qy 1397 GAGTCTGCTGCCACAGGTGACACGCTCTCAGGGAAGAAGATATGACGTCTCTACCTGG 1456
Db 1430 ACCTGCTGCCACCGGTTACAGGACITGATGGAGGCCACCTATACAGTGTCTCATTTG 1489
Qy 1457 GGACAGAGGATGGACACCTCCACCGGGCTGTGGCATTGGAGCTCAGCTCAGTGTCTTGG 1516

Db 1490 GCACAGAGAGCGCTGGCTGCTCAAGGCTGTGAGCCCTGGGGCCCTGGGTTCACTGATTG 1549
Qy 1517 AGGATCTGGCTTGT--CCAGAACACAGCGGTTGAGAGCATGAATTTGACACG 1573
Db 1550 AGAGCTGACGCTGTTGACACAGAGCCCATGAGACCTGGTGTATCTCAGAGCAAGA 1609
Qy 1574 ATTGGCTCCTGGGCTCCACTACTAGAGTGACACAAAGTGAACACACAGCAACTGTGGCC 1633
Db 1610 AGCTGCTCTTGGCGGCTCCGCTCTCAGCTGGTGCAGCTGCCGTGGCGGACTGCATAA 1669
Qy 1634 GTCTCAGAGCTGCTGGAGTGTATCTTGGCCCGCAGGACCCGCTGGCGCTGAGCTTCC 1693
Db 1670 AGTATCGCTCCTGTGCAGACTGTCTCTCGCCGGGACCCCTATTGGCGCTGGAGCGTCA 1729
Qy 1694 GGCTTGATGCTGTGTGGCCACCGCGGCA 1724
Db 1730 ACACAGCCCGCTGTGTGGCCGTGGTGGCCA 1760

RESULT 9
US-10-002-304-11
; Sequence 11, Application US/10002304
; Publication No. US20030036185A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meljia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: Polynucleotides and polypeptides encoded thereby
; FILE REFERENCE: 15966-554 Cura-54 CON-S8
; CURRENT APPLICATION NUMBER: US/10/002,304
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 2155
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (166)..(1935)
US-10-002-304-11

Query Match 6.2%; Score 248.6; DB 14; Length 2155;
Best Local Similarity 52.1%; Pred. No. 5.4e-58;
Matches 704; Conservative 0; Mismatches 629; Indels 18; Gaps 6;

Qy 383 GAGGATCGACTGGATGTTACCTGAGACTCACAGACAGAACTCGAGGAAGAGGCAAG- 441
Db 419 GAGCGATCTCTGGGAGGCCCCCGTGGAGAAGAAGACTAGTGTATCCAGAAAGGAAGA 478
Qy 442 --AAAGAGGAGATGCAAAATTTATCCAGATTCTCGCCATTGTGAATGCCCTCTACC 499
Db 479 ACACACCGGAGTGTCTCAACTTCATCGCTCTCTCGAGCCCTACAATGCCCTCCACC 538
Qy 500 TCCTCAGCTGGGCACCTTCGCTTTTATCCGAAGTGGCGGGTTATTGATGTGTCACAGTT 559
Db 539 TGTACGCTGTGGCACCTACGCCCTCCAGCCCAAGTGCACCTACGTCACATGCTCACT 598
Qy 560 TCCA---GCAGTTTGAAGACTTGAAGCGCGCGGGAATATGTCCTTTTGAAGCCAGCTC 616
Db 599 TCACCTTGGAGCATGGAGAGTTTGAAGATGGGAAGGCAAGTGTCCCTATGACCCAGCTA 658
Qy 617 AACGGTCAGCAGCTGTAATGGCTGGGGGGCTCTCTACACCGGCCACTGTGAAGAACTTCC 676
Db 659 AGGCCCATGTGGCCCTTCTTTGTGATGGTGTAGCTGTACTCGGGCCACACTCAACAACTTCC 718

Qy 677 TGGGGACTGAGCCATCATCTCCGAGCTGTGGGTGAGCTGAGGACTGATTCGAACAG 736
Db 719 TGGCAGGAAACCATATTCTCGTAAACATGGGC--CCACCACTCCATGAAGACAG 775
Qy 737 AGACCTTGTCTATCTGGCTTAAATGCTCCAGCCCTTGTGCGAGCTATGCTCCTGAGCCAG 796
Db 776 AGTACCTTGGCTTTGGCTCAAGCAACCTCACTTTGTAGGCTTGCCTATGCTACCTGAGA 835
Qy 797 CTGAGTGGGGGATGAAGATGGAGACGATCAAAATCTTTTCTTCTCAGGAGACCTCC 856
Db 836 GTGTGGGACGCTTACGGGGGACGACAAAGGTCTACTTCTTCTCAGGAGGGGCGAG 895
Qy 857 GAGTGTGGGACTCTATGAGCGCATCAAGTCCCAAGAGTGGCCGAGTGTGTGCGGGG 916
Db 896 TGGAGTCCGACTGCTATGCCGAGCAGGTGTGCTGTGGCCGCTGTGCAAGGGCG 955
Qy 917 ACCTTGGGGCAGAAAGACCTTTCAGCAGAGATGGAGCAGCTTTCTGAAGGCTGACCTGC 976
Db 956 ATATGGGGGCGCAGGACCTTGCAGAGAAAGTGGACACGTTCTTCAAGCGCGGCTGG 1015
Qy 977 TGTGCCAGGGCCGAGCATGGCGGGCTCCGGGTTCTGCAAGGCTATGCGAGGCTTC 1036
Db 1016 CATGCTCTGCCCGAACTGGCAGCTTACTTCAACAGCTGCGAGCGATG---CACACCC 1072
Qy 1037 GGCTCAGCCTGGAGCGGGAACCCCATCTTTTATGGATCTTTTCTCCAGTGGGAAG 1096
Db 1073 TGCAGGACACCTCCTGGCACAACACACCTTCTTGGGGTTTTCAGACGACAGTGGGGTG 1132
Qy 1097 GAGCTGCCATCTCTGCTGTGTGCTTCCAGACCCCAAGACATCCGGGGCAGTGTCTGAATG 1156
Db 1133 ACATGTACCTGTGGCCATCTGTAGTACCAGTTCAGAGAGATGACAGCGGCTGTTGAGG 1192
Qy 1157 GTCCCTTAGAGAGCTAAACATGACTGCAACAGGGGACTGCCTGTCTATGCAACACAGG 1216
Db 1193 GCCCTATAAGGAGTACCATGAGGAGCCCAAGTGGGACCGGTACACTGACCT--G 1249
Qy 1217 TGCCCCAGCCAGACCTTGGAGAGTGCATCGCCAAACAACTGAAGTCCAGCAGTTTGGAT 1276
Db 1250 TACCCAGCCCTCGGCTGGCTGTGCTGCAATTAACAACCTGCGATCGCGCCACGGCTACACCA 1309
Qy 1277 CCTCCTCTCCCTGCCAGACCGGCTGTCTACCTTTATCAGAGACACCCCTCTCATGAGCA 1336
Db 1310 GCTCCTTGGAGCTACCGCAACATCTCAACTTCGTCAGAGACACCCGCTGATGGAGG 1369
Qy 1337 GGCCCGTTCCTGGCTGACGGCGCCCTGCTGCTACTACAGATACAGCCTATCTCA 1396
Db 1370 AGCAGTGGGGCTCGGTGAGCGCCCTGCTGCTGGAAGAGGGCAACCACTTCACCC 1429
Qy 1397 GAGTCTGGCCCGCAGGGTGACAGCCTCTCAGGGAAGAATATGAGCTGCTCTACCTGG 1456
Db 1430 ACCTGGTGGCGGACCGGTTACAGGACTTGTATGAGCCACCTATACAGTGTGTTCAATTG 1489
Qy 1457 GGCAGAGAGATGAGACACTCCACGGGCTGTGGCATTTGAGAGTACAGTCACTGCTGTTGG 1516
Db 1490 GCACAGGAGCGGCTGCTCAAGGCTGTGAGCCTTGGGGCCCTGTTGCTGCTGATG 1549
Qy 1517 AGGATCTGGCTTGT--CCAGAACACAGCGGTTGAGAGCATGAAATGTTACACAG 1573
Db 1550 AGGAGCTGACGCTGTTTGACACGAGGCGCCATGAGACCTGCTGCTATCTCAGAGCAAGA 1609
Qy 1574 ATTGGCTCCTGGTGGCTCCCTACTAGGTGACACAAAGTGAACACCACTGCTGGCC 1633
Db 1610 AGCTGCTCTTGGCGGCTCCGCTCTCAGCTGGTGTGAGCTGCCGTGCCGAGCTGCATAA 1669
Qy 1634 GTCTCAGAGCTGCTGGAGTGTATCTTGGCCCGCAGGACCCGCTGTGGCCCTGAGCTTCC 1693
Db 1670 AGTATCGCTCCTGTGCAGACTGTCTCTCGCCGGGACCCCTATTGCGCTGGAGCGTCA 1729
Qy 1694 GGCTTGATGCTGTGTGGCCACCGCGGCA 1724
Db 1730 ACACAGCCCGCTGTGTGGCGCTGGTGGCCA 1760

RESULT 10

US-10-003-152-21
; Sequence 21, Application US/10003152
; Publication No. US20020151494A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meljia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: No. US20020151494A1el Amino Acid Sequences for Human Semaphorin-1
; FILE REFERENCE: 15966-554 Cura-54 CON-S12
; CURRENT APPLICATION NUMBER: US/10/003.152
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604, 286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140, 584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 2156
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (166)..(2037)
; NAME/KEY: Variation
; LOCATION: (1)..(2156)
; OTHER INFORMATION: N may be any nucleotide
US-10-003-152-21

Query Match 6.2%; Score 248.6; DB 13; Length 2156;
Best Local Similarity 52.1%; Pred. No. 5.4e-58;
Matches 704; Conservative 0; Mismatches 629; Indels 18; Gaps 6;

QY	383	GAAGGATCGACTGGATGCTGAGACTCAGACACAACTGAGGAGAAAGCAAG- 441
DB	419	GAGCGATCTCTGGGAGCCCGCTGGGAGAGAGACTGAGTGATCCAGAAGGAGA 478
QY	442	--AAGAGGACATGTACAAATTTATCCAGATCTCGCCATGTCAATGCCTCTACC 499
DB	479	ACAACGACGAGGTGCTTCAACTTCATCCGCTTCTCGACGCCCTACAAATGCCTCCACC 538
QY	500	TCCTCAGCTGGGACCTTCGCTTTGATCCGAAGTGGGGTTATTGATGTGCCAGTT 559
DB	539	TGTAGCTGTGGGACCTTACGCCCTTCCAGCCCAAGTGCACTAGCTCAACATGCTACCT 598
QY	560	TCCA---CGAGTTGAAGACTTGAGAGCGCGGGGAAATGTCTTTTGAGCGCAGCTC 616
DB	599	TCACCTTTGAGCATGGAGAGTTTGAAGATGGGAAGGCAAGTGTCCCTATGACCCAGCTA 658
QY	617	AACGGTCAAGAGCTGTAATGCTGGGGGGCTCTCTACACCGCACTGTGAAGAACTTCC 676
DB	659	AGGGCCATGCTGGGCTTCTTGTGATGTGAGCTGTACTCGGCCACACTCAACAATTC 718
QY	677	TGGGACTGAGCCCATCATCTCCGAGCTGTGGTGGTGGAGCTGAGGACTGGATTGCAACAG 736
DB	719	TGGGACCGAAGACCATATATCTCGGTAACTATGATGGGGC---CCACACACTCCATGAAGACAG 775
QY	737	AGACCTTGTATCTCTGGCTTAATGCTCCAGCCTTTGTGCGAGCTATGGTCTCGAGCCCAAG 796
DB	776	AGTACCTGGCCCTTTTGGCTCAACGAACCTCACTTTGTAGGCTCTGCCTATGTACTTACCTGAGA 835
QY	797	CTGAGTGGGGGATGAAGATGGAGCATGAAATATCTTTTCTTCTACGGAGACCTTCC 856
DB	836	GTGTGGGAGCTTTCACGGGGGACGACGAAAGTCTACTTCTTCTCAGGGAGCGGGCAG 895
QY	857	GAGTGTGGGACTCTATGAGCGCATCAAGGTCCCAAGAGTGGCCCGAGTGTGCGGGGG 916
DB	896	TGGAGTCGCACTGTATATGCCAGGAGGTGGTGGCTCGTGTGGCCCGCTGTGCAAGGCGC 955

QY	917	ACCTTGGGGGAGGAAGACCTTTCAGCAGAGATGACGACGTTTCTGAAGGCTGACCTGC 976
DB	956	ATATGGGGGGCGCAGCGACCTCGCAGAGGAAGTGACACAGTTCCTGAAGCGCGCGCTGG 1015
QY	977	TGTGCCAGAGGGCCGAGCATGGCCGGGCTCTCGGGGGTTCGCGAGGCTATGGCAGAGCTTC 1036
DB	1016	CATGCTCTGCCCGCAACTGGCAGAGTCTACTTTCAACACAGCTGCGAGCGATG---CACACC 1072
QY	1037	GGCCTCAGCCCTGGAGCGGGAACCCCATCTTTTATGGGATCTTTTCCCTCCAGTGGGAAG 1096
DB	1073	TGCAGGACACCTCTCTGGCACAACACACCTCTTTTGGGGTTTTTCAACACAGTGGGGTG 1132
QY	1097	GAGTGGCATCTCTGCTGTGTGCTTCCGACCCCAAGACATCCGGGCGAGTGCCTGAATG 1156
DB	1133	ACATGTACCTCTGCGCCCATCTGTGAGTACCAGTTTGGAGAGATCCAGCGGCTGTTGAGG 1192
QY	1157	GTCCTTTTAGAGAGCTAAACATGACTGCACAGGGGACTGCTGTCTATGGAACACGAGG 1216
DB	1193	GCCCTATATAGGAGTACCATGAGGAAGCCCAAGAGTGGGAGCGGCTTACACTGACCCCT---G 1249
QY	1217	TGCCCCAGCCAGACCTGGAGAGTGCATCGCCCAACACATGAAGCTCCAGCAGTTTGGAT 1276
DB	1250	TACCCAGCCCTCGGCTGGCTGCTGCAATTAACAACCTGGCATCGGGCGCCACGGCTACACCA 1309
QY	1277	CCTCACTCTCCCTGCCAGACCGGCTGCTCACTTTTATCAGAGACACACCTCTCTCATGGACA 1336
DB	1310	GCTCCCTGGAGTACCCGACAAACATCTCAACTTCGTCAAGNAGCACCCTGATGGAGG 1369
QY	1337	GGCCGCTGTTCCCGGCTGACGGCGGCCCCCTGCTGGTGCATACAGATACAGCCTATCTCA 1396
DB	1370	AGCAGGTGGGCGCTCGGTGGAGCGCGCCCTCTGCTGTAAGAAGGCGCACTTCACTCC 1429
QY	1397	GAGTCGTGGCCACAGGCTGACAGCCCTCTCAGGGAAGAAATATGACCTGCTCTACCTGG 1456
DB	1430	ACCTGGTGGCGACCGGCTTACAGACTTGATGGAGCCACCTATACAGTGTCTGTTCAATTG 1489
QY	1457	GGACAGAGATGGACACCTCCACCGGCTGTGCGCATTTGGAGCTCAGCTCAGTGTCTTGG 1516
DB	1490	GCACAGGAGACGGCTGGCTGCTCAAGGCTGTGAGCCTGGGCGCTTCACTGATG 1549
QY	1517	AGGATCTGGCCCTGTT---CCAGAACACACCGCGTTGAGAGCATGAAATTTGATACCAG 1573
DB	1550	AGGAGCTGCAGCTGTTTGACCAAGAGGCCCATGAGAAGCCTGTGCTATCTCAGAGCAAAA 1609
QY	1574	ATTGGCTCTGCTGGGCTCCCATCTAGAGTGACAAAGTGAACACCACTGCTG6CC 1633
DB	1610	AGCTGCTCTTTGCGGCTCCCGCTCTCAGCTGGTGCAGCTGCCGTGGCCGCACTCATTA 1669
QY	1634	GTCTCCAGAGCTGCTCGGAGTGTATCTTGGCCCAAGGACCCGCTGTGCGCTTGGAGCTTCC 1693
DB	1670	AGTATCGCTCTGTGCGAGACTGTGCTCTCGCCCGGAGCCCTCTATTGCGCCTGGAGCGTCA 1729
QY	1694	GGCTTGATGCTGTGTGGCCCAACCGCGCGA 1724
DB	1730	ACACGAGCGCTGTGTGGCCGTGGGTGGCCA 1760

RESULT 11

US-10-002-050-21
; Sequence 21, Application US/10002050
; Publication No. US20030032095A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meljia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: No. US20030032095A1el Nucleic Acid Sequences Encoding Human Se
; FILE REFERENCE: 15966-554 Cura-54 CON-S14
; CURRENT APPLICATION NUMBER: US/10/002.050
; CURRENT FILING DATE: 2001-11-02

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; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 2156
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (166)..(2037)
; NAME/KEY: variation
; LOCATION: (1)..(2156)
; OTHER INFORMATION: N may be any nucleotide
US-10-002-050-21

Query Match          6.2%; Score 248.6; DB 14; Length 2156;
Best Local Similarity 52.1%; Pred. No. 5.4e-58;
Matches 704; Conservative 0; Mismatches 629; Indels 18; Gaps 6;

Qy 383 GAAGGATCGACTGGATGGTACCTGAGACTCACACAGAACTGCAGGAAGAAAGGCAAG- 441
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 419 GAGGATCTCTCTGGGAGGCCCCCGTGGAGAAGAACTGAGTGTATCCAGAAGGGGAAGA 478
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 442 --AAAGAGGAGCAATGCAAAATTTATCCAGATTCTCGCCATTGTCAATGCCCTCTCAC 499
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 479 ACAACGAGCCGAGTGTCTCAACTTCATCCGCTCTCTGAGCCCTACAATGCCCTCCACC 538
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 500 TCCTCAGCTGGGCACTTCGCTTTTGTATCCGAATGCGGGGTTATGATGTCCTCAGTT 559
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 539 TGTACGCTGTGGCACCCTACGCTTCCAGGCCCAAGTGCACCTACGTCGAACATGCTCAC 598
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 560 TCCA--GCAGGTGAAGACTTGAGAGCGCGCGGGGAATGTCCTTTTTCAGCCAGCTC 616
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 599 TCACCTTTGGAGATGGAGAGTTTGAAGATGGGAAGGCAAGTGTCCCTATGACCCAGCTA 658
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 617 AACGGTCAGCAGCTGTATAGCTGGGGCGCTCTCTACACGCCACTGTGAAGAACTTCC 676
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 659 AGGCCATGCTGGCCCTTCTGTGATGTTGAGCTGTACTCGGCCACACTCAACAACTTCC 718
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 677 TGGGAGTGAAGCCCATCATCTCCCGAGCTGTGGTGCAGCTGAGGATGGAATGCAACAG 736
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 719 TGGCAGCGGAACCCATATCTCGCTAATCTGCTAATCTGAGTGGG--CCACCACTCCATGAAGACAG 775
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 737 AGACCTTGTCATCTGCTTAATCTCCAGCCTTTGTCGACGCTATGCTGAGCCAG 796
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 776 AGTACCTGGCCTTTTGGCTCAACGAACCTCACTTTGTAGGCTCTGCTATGACTGAGA 835
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 797 CTGAGTGGGGGATGAAGATGGAGACGATGAAATCTTTTCTTTCACGGAGACCTCC 856
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 836 GTGTGGCAGCTTTCACGGGGACGACACAGGTCTACTTCTTTCAGGGAGCGGGCAG 895
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 857 GAGTGTGGAGTCTCTATGAGCGCATCAAGTTCACAGAGTGGCCGCGGAGTGTGCGGGG 916
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 896 TGGAGTCCGACTGTATGCCAGCAGAGGTGTGTGCTGTGCGCCGCTGTCTCAAGGCG 955
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 917 ACCTTGGGGCAGGAAGACCTTTCAGCAGAGATGGAGCAGCTTTCTGAAGCTGACCTGC 976
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 956 ATATGGGGGGCGCAGCAGCCCTGACAGAGAAAGTGCACCCAGCTTCTTGAAGCGCGGTG 1015
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 977 TGTGCCAGGCGCCGAGCATGGCGGCTCCGGGTTCTGACGAGCTATGCAGAGCTTC 1036
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1016 CATGCTTGCCCCGAACTGGCAGCTCTACTTCAACACAGCTGCAGCGCATG--CACACC 1072
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1037 GGCTCAGCTTGGAGCGGGAACCCCATCTTTTATGGATCTTTTCTCCAGATGGGAAG 1096
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1073 TGCAGGACACCTCTCTGGCACAACACCACTTCTTTTGGGGTTTTCAGACAGCTGGGGTG 1132
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1097 GAGTGGCATCTCTGCTGTGTGCTTCCGACCCCAAGACATCCGGCAGTGTGATG 1156
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1133 ACATGTACCTGTGCGGCATCTGTGAGTACCAGTTTGAAGAGATCCAGCGGTGTTGAGG 1192
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT 12
US-10-002-304-21
; Sequence 21, Application US/10002304
; Publication No. US20030036185A1
; GENERAL INFORMATION:
; APPLICANT: Shinkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meijia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: Polynucleotides and polypeptides encoded thereby
; FILE REFERENCE: 15966-554 Cura-54 CON-S8
; CURRENT APPLICATION NUMBER: US/10/002.304
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 2156
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (166)..(2037)
; NAME/KEY: variation
; LOCATION: (1)..(2156)
; OTHER INFORMATION: N may be any nucleotide
```

US-10-002-304-21

Query Match	6.2%	Score 248.6	DB 14	Length 2156
Best local similarity	52.1%	Pred. No. 5.4e-59		
Matches 704	Conservative 0	Mismatches 629	Indels 18	Gaps 6
QY	383	GAAGGATCGACTGGATGGTACCTGAGACTCACAGACAGAAGCTGCAGGAAGAAAGGCAAG- 441		
DB	419	GAGCGATCTCTGGGAGGCCCGCTGGAGAAGAGACTGAGTGTATCCGAAGAGGGAAGA 478		
QY	442	--AAAGAGGACGAATGTACAATTTTATCCAGATTCTTCGCCAATGTGCAATGCCTCTCACCC 499		
DB	479	ACAACCAGACCGAGTGTCTCAACTTCATCCGCTTCTGCGACGCTCAATAGCTCTCCCAACC 538		
QY	500	TCCTCAGCTCGGCACCTTCGCTTTTCATCCGAAGTCGCGGGTATTGATGTGTCCAGTT 559		
DB	539	TGTACGTCTGTGCACCTACGCTTCCAGGCCCAAGTCACCTACGTCACCAATGCTCACT 598		
QY	560	TCCA--GCGAGTTGAAAGACTTGCAGAGCGCCGGGAAATGCTCTTTTGAGCCAGCTC 616		
DB	599	TCACTTTGGAGCATGGAGACTTTGAAGATGGGAAGGCAAGTGTCCCTATGACCCAGCTA 658		
QY	617	AAGCGTCAGACGTGTAATGGCTGGGGGCTCTCTACACGGCAGCTGTGAAGACTTCC 676		
DB	659	AGGGCCATGCTGGCCTCTTGTGGATGGTGAAGTGTACTCGGCACACTCAACAACCTTCC 718		
QY	677	TGGGGACTGAGCCCATCATCTCCCGAGCTGTGGTGCAGCTGAGGACTGATTCGACAC 736		
DB	719	TGGGACGGAACCAATATCTCGGTACATGGGGC---CCACCACTCCCTGAAGACAG 775		
QY	737	AGACCTTGTTCATCTCGCTTAATGCTCCAGCCTTTGTGCGAGCTATGGTCTCAGCCAC 796		
DB	776	AGTACCTGGCCTTTTGGCTCAACGAACCTCACTTTGTAGGCTCTGCTCATGTACCTGAGA 835		
QY	797	CTGAGTGGGGGATGAGATGGAGACGATCAAAATCTTTTTTTTCTTCCACGGAGACCTCCC 856		
DB	836	GTGTGGGCAGCTTCACGGGGGACGACGAAGGTCCTACTTCTTTCAGGGAGCGGGCAG 895		
QY	857	GAGTGTGTGGACTCCTATGAGCGCATCAAGGTCCCAAGAGTGGGCCGAGTGTGCGGGGG 916		
DB	896	TGGAGTCCGACTGCTATGCCGAGCAGGTGCTGCTGTGGCCGTGTCTGCAAGGGCG 955		
QY	917	ACCTTGGGGCAGGAAGACCCCTTCAGCAGAGATGGAGCAGTTCGTGAAGGCTGACCTGC 976		
DB	956	ATATGGGGGGCCACGGACCCCTCAGAGGAAGTGGACAGTTTCTTGAAGCGCGGCTGG 1015		
QY	977	TGTGCCCAGGGCCGAGCATGGCCGGGCTTCGAGGGTCTTCGAGGCTATGGCAGAGCTTC 1036		
DB	1016	CATGCTCTGCCCGAACTGCGAGCTCTACTTCAACAGCTTCGAGGCGATG---CACACC 1072		
QY	1037	GGCCTCAGCCTGGAGGGGAACCCCATCTTTTATGGGATCTTTTCTCCAGTGGGAAG 1096		
DB	1073	TGCAGGACACCTCCTGBCACAACACCCTTCTTTGGGGTTTTTCAAGCACAGTGGGGTG 1132		
QY	1097	GAGCTGCCATCTCTGTGTGTGTGCTTCGACCCCAAGACATCCGGGCACTGCTGATG 1156		
DB	1133	ACATGTACCTGTCTGGGCATCTGTGAGTACCAGTTGGAAGAGATCCAGCGGGTGTGTGAGG 1192		
QY	1157	GTCCCTTTAGAGAGCTAAACATGACTGCAACAGGGGACTGCTCTCATGGCAACAGG 1216		
DB	1193	GCCTCTATAGGAGTACCATGAGGAAGCCAGAAGTGGGACCGCTACACTGACCT---G 1249		
QY	1217	TGCCCCAGCCCACTGGAGATGATGCCCAACAAACATGAAGCTCCACGACTTTGGAT 1276		
DB	1250	TACCCAGCCCTCGCCTGGCTCGTGTGATTAACAACTGGCATCGCGGCCAGGGGTACACCA 1309		
QY	1277	CCCTCACTCTCCCTGCCAGACCGGTGCTCACTTTTATCAGAGACCAACCCCTCTCATGGACA 1336		
DB	1310	GCTCCCTGGAGCTACCCGACAACTCTCAACTTGTCTCAGAGACACCCGCTGATGGAGG 1369		
QY	1337	GGCCCGTGTTCGGGTGACGGCCGCCCTGCTGTGCTACTACAGATACAGCCTATCTCA 1396		
DB	1370	AGCAGTGGGGCTCGGTGGAGCGGCCCTGCTGCTGTGAAGAGGGCACCACCTCTCACCC 1429		

Qy 1397 GAGTCGTGGCCACAGGGTCACACAGCCTCTCAGGGAAAGAAATATGACGTGCTCTACCTGG 1450

Db 1430 ACCTGTGTGGCGACCGGGTTACAGAGACTTGATGGAGCCACCTATACAGCTGCTGTTTCATTG 1489

Qy 1457 GGACAGAGGATGACACACTCACCGGGCTGTGGCGATTGGAGCTCAGCTCAGTGTCTTTGG 1516

Db 1490 GCACAGAGAGCGCTGGCTGCTCAAGGCTGTGAGCCTGGGGCCCTGGGTTCACTGATTTG 1549

Qy 1517 AGGATCTGGCCTTGTGTT---CCCAGAACACAGACCGCGGTGTGAGACGATGAAATTTGACACAG 1573

Db 1550 AGGAGCTGCAGCTGTTTGACAGGAGGCCATGAAAGCCCTGGTGCTATCTCAGAGCAAAA 1609

Qy 1574 ATTGGCTCCTGTGGGGCTCCCATCTAGGTGACACAGTGAACACACCACTGTGGCC 1633

Db 1610 AGCTGCTCTTTGGCGGCTCCCGTCTCAGCTGTGTGAGCTGCGCGGTGGCGAGTGCATT 1669

Qy 1634 GTCTCCAGAGCTGCTGGAGTGTATCTGTGCCACGAGACCCCGTGTGGCGTGGCGAGTGCATT 1729

Db 1670 AGTATCGTCTCTGTGCAGACTGTGTCTCGCCCGGAGACCCCTATTGGCGCTGGAGCGTCA 1729

Qy 1694 GGCTTGATGCTTGTGGGGCCACCGCGGCA 1724

Db 1730 ACACGAGCCTGTGTGGCGGTGGCGCA 1760

RESULT 13

US-10-003-152-13

; Sequence 13, Application US/10003152

; Publication No. US20020151494A1

; GENERAL INFORMATION:

; APPLICANT: Shimkets, Richard

; APPLICANT: Fernandes, Elma

; APPLICANT: Vernet, Corine

; APPLICANT: Yang, Meljia

; APPLICANT: Boldog, Ferenc

; APPLICANT: Herrmann, John

; TITLE OF INVENTION: No. US20020151494A1e1 Amino Acid Sequences for Human Semaphorins

; FILE REFERENCE: 15966-554 Cura-54 CON-S12

; CURRENT APPLICATION NUMBER: US/10/003,152

; CURRENT FILING DATE: 2001-11-02

; PRIOR APPLICATION NUMBER: 09/604,286

; PRIOR FILING DATE: 2000-06-22

; PRIOR APPLICATION NUMBER: 60/140,584

; PRIOR FILING DATE: 1999-06-23

; NUMBER OF SEQ ID NOS: 49

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 13

; LENGTH: 2284

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (166)..(1953)

; NAME/KEY: variation

; LOCATION: (1)..(2284)

; OTHER INFORMATION: N may be any nucleotide

; US-10-003-152-13

	Query Match	6.2%	Score 248.6;	DB 13;	Length 2284;
	Best Local Similarity	52.1%	Pred. No. 5.5e-58;		
	Matches 704;	Conservative	0;	Mismatches 629;	Indels 18; Gaps 6;
Qy	383	GAAGGATCGACTCGATGGTACCTGAGACTCACAGACAGAACTCAGAGAAAGGCAAG-	441		
Db	419	GAGCGATCTCTGGGAGGCCCGCTGGAGAAAGAACTGAGTGTATCCAGAAAGGGAAGA	478		
Qy	442	--AAAGGAGCAGAAATGTCACAATTTTATCCAGATTTCTGCCCATTTGCTCAATGCCTCACC	499		
Db	479	ACAACAGACCGAGTGTCTCAACTTATCGCTTCTCGAGGCCATTACAATGCTCCCAAC	538		
Qy	500	TCCTCAGTCGCGCAGCTTCGCCTTTTGATCCGAAGTCGGGGTTATTGATGTGTCAGATT	559		

Db 539 TGTACGTCTGTGGCAACCTACCCCTTCCAGGCCAAGTGCACCTACATCAACATGCTCACT 598
Qy 560 TCCA---CGAGTTGAAGACTTTCAGAGCGCCGGGGAATATGCTTTTCAGCCAGCTC 616
Db 599 TCACCTTTGGACATGGAGAGTTTGAAGATGGGAAGGCAAGTGTCCCTATGACCACGCTA 658
Qy 617 AACGGTCAGCAGCTGTATATGCTGGGGCGTCTCTACACCGCCACTGTGAAGAACTTCC 676
Db 659 AGGGCCATGCTGGCCCTCTCTGTGGATGGTGAAGTGTACTCGGCCACACCTCAACAACCTCC 718
Qy 677 TGGGACTAGCCCATCATCTCCGAGCTGTGGTGCAGCTGAGGACTGGATTGCAACAG 736
Db 719 TGGGACAGGAACCATATTATCTGCTAACATGGGGC---CCACCACTCCATGAAGACAG 775
Qy 737 AGACCTTGTCTATCTGGCTTAATGCTCCAGCCTTTGTCGACGCTATGCTGAGCCGAG 796
Db 776 AGTACCTGGCCCTTTTGGCTCAACGNACTCACTTTGTAGGCTCTGCCCTATCTACCTGAGA 835
Qy 797 CTGAGTGGGGGATGAAGATGGAGCAGTGAATCTTTTTCACGAGGACCTCC 856
Db 836 GTGTGGGAGCTTCACGGGGGACGACGACAAAGTCTACTTCTTTCAGGAGCGGGCAG 895
Qy 857 GAGTGTGGACTCTATGAGCGCATCAAGTCCCAAGAGTGGCCGAGTGTGCGGGG 916
Db 896 TGGAGTCGAGTCTATGACGAGAGTGGTGGCTGCTGTGGCCGCTGTCTGCAAGGGCG 955
Qy 917 ACCTTGGGGGAGGAAGACCTTCAGCAGAGATGGACGAGCTTTCTGAAGCTGACCTGC 976
Db 956 ATATGGGGGCGACGACCTTCAGAGGAGTGGACCACTGCTTCTGAAGCGGGCTGG 1015
Qy 977 TGTGCCAGGGCCGAGCATGCGCGGGCTCCGGGTTCTCAGGCTATGACAGCTTC 1036
Db 1016 CATGCTGCGCCGAACTGGCAGCTCTACTTCAACCACTGCGGCGATG---CACACCC 1072
Qy 1037 GGCCTCAGCTGGAGGGGAACCCCATCTTTTATGGATCTTTTCTCCAGAGTGGAG 1096
Db 1073 TGCAGGACACCTCTCTGGCACAACACACCTTTCTTTGGGTTTTCAGACAGCTGGGTG 1132
Qy 1097 GAGCTGCATCTCTGCTGTGTGCTTCCGACCCCAAGACATCGGGCAGTGTGAATG 1156
Db 1133 ACATGTACCTGTGGCCATCTGTGATACCACTTGGAGAGATCCAGCGGTGTTGAGG 1192
Qy 1157 GTCCCTTTAGAGATAAATCATGACTGCAACAGGGGACTGCTCTCATGGAACACGAG 1216
Db 1193 GCCCTATAGAGAGTACCATGAGGAAGCCAGAAAGTGGGACCGGTACACTGACCT---G 1249
Qy 1217 TGCCCCCAGCCAGCTGGAGAGTGCATCGGCCACACATGAAGCTCCAGCACTTTGGAT 1276
Db 1250 TACCCAGCCCTCGGCCCTGGCTCGTGCATTAACAACCTGGCATCGGCCGACCGGCTACACCA 1309
Qy 1277 CCTCACTCTCCGACAGCCGCTGCTCACTTTATCAGAGACACCCCTCTCATGGACA 1336
Db 1310 GCTCCTGGAGCTACCCGACAACATCTCACTTCTGTCGAAGAACCCCGCTGATGGAG 1369
Qy 1337 GGGCCGCTTCCGGCTGACGGCCGCGCCCTGCTGGTCACTACAGATACAGCCCTATCTCA 1396
Db 1370 AGCAGGTGGGCGCTCGGTGGAGCGCCGCTGCTGTAAGAGGGCAACCACTTCACCC 1429
Qy 1397 GAGTCGTGGCCCAAGAGTACAGCCCTCTCAGGGAAGAATATGACGTCTACCTGG 1456
Db 1430 ACCTGGTGGCGGACCGGTTACAGGACTTGTAGGACCCACCTATACAGTGTGTTCAATTG 1489
Qy 1457 GGACAGAGATGAGACATCCACCGGCTGTGGCATTTGAGCTGAGCTCAGTGTCTTGG 1516
Db 1490 GCACAGGAGCGGCTGGCTGCTCAAGGCTGTGAGCCTGGGGCCCTGGGTTTCACTGATTG 1549
Qy 1517 AGGATCTGGCCCTTGT---CCAGAAACACAGCCGCTTGGAGAGCATGAATTTGACACAG 1573
Db 1550 AGGAGCTGCACTGTTTGAACAGGAGCCATGAGAGCCTGGTCTATCTCAGAGCAAGA 1609
Qy 1574 ATTGGCTCCTGGTGGGCTCCCATACTAGGTGACACAAAGTGAACACCAAGCACTGTGCC 1633
Db 1610 AGCTGCTCTTTGGCGGCTCCCGCTCTCAGCTGGTGCAGCTGCCGCTGGCCGACTGCATAA 1669

RESULT 14

US-10-002-050-13
; Sequence 13, Application US/10002050
; Publication No. US20030032095A1
; GENERAL INFORMATION:
; APPLICANT: Shinkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Melija
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: No. US20030032095A1el Nucleic Acid Sequences Encoding Human Se
; FILE REFERENCE: 15966-554 Cura-54 CON-514
; CURRENT APPLICATION NUMBER: US/10/002,050
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 13
; LENGTH: 2284
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (166)..(1953)
; NAME/KEY: variation
; LOCATION: (1)..(2284)
; OTHER INFORMATION: N may be any nucleotide
US-10-002-050-13

Query Match 6.2%; Score 248.6; DB 14; Length 2284;
Best Local Similarity 52.1%; Pred. No. 5.5e-58;
Matches 704; Conservative 0; Mismatches 629; Indels 18; Gaps 6;

Qy 383 GAAGATCGACTGGATGTTACTGAGACTCACAGACTGACAGAACTGCGAGGAAGGCAAG- 441
Db 419 GAGCGATCTCCTGGGAGGCCCGCTGGAGAAGAGACTGAGTGTATCCAGAAGGGAAGA 478
Qy 442 --AAGAGGACGAATGTCACAAATTTATCCAGATTCTGCCATTCTCAATGCTCTCACC 499
Db 479 ACAACAGACCGAGTGTCTCAACTTCATCCGCTTCTCGAGCCCTACATGCTCCACACC 538
Qy 500 TCCTCACCTCGGGACCTTCGCTTTTGATCCGAAGTGGGGGTTATGATGTGTCAGTT 559
Db 539 TGTAGCTGTGGCCACTACGCTTCCAGCCCAAGTGCACCTACATGCTCACTCACCCT 598
Qy 560 TCCA---CGAGTTGAAAGACTTGAGAGCGCCGGGGAATGTCTTTTGTAGCCAGCTC 616
Db 599 TCACCTTGGAGCATGGAGAGTTTGAAGATGGGAAGGCAAGTGTCCCTATGACCCAGCTA 658
Qy 617 AACGTCAGCAGCTGTAATGGCTGGGGGCTCTCTACACCGCCACTGTGAAGAACTTCC 676
Db 659 AGGGCCATGCTGGCCCTTCTTGTGGATGGTGAAGTGTACTCGGCCACACTCAACAACCTTCC 718
Qy 677 TGGGACTGAGCCCATCATCTCCGAGCTGTGGGTCGAGCTGAGGACTGGATTCCGAACAG 736
Db 719 TGGGACCGGAACCCATTATCTGCTGAACATGGGGC---CCACCACTCCATGAAGACAG 775
Qy 737 AGACCTTGTCTCTGCTTAATGCTCCAGGCTTTGTCGCACTATGCTGCTGAGCCGAG 796

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Db 776 AGTACTGCGCTTTTGGGCTCAACAGACCTCACTTTGTAGGCTCTGCTTATGACTGAGA 835
QY 797 CTGAGTGGGGGATGAAGATGAGACGATGAATCTTTTCTTCTACGGAGACCTCC 856
Db 836 GTGTGGGAGCTTACGGGGACGACGACAAAGTCTACTTCTTCTCAGGGAGCGGCAG 895
QY 857 GAGTGTGGACTCTATAGACGCATCAAGGTCCCAAGAGTGGCCCGAGTGTGTGGGGG 916
Db 896 TGGAGTCCGACTATATCGGAGCAGGTGTGGCTCGTGTGGCCCGTGTCTCAAGGGG 955
QY 917 ACCTTGGGGCAGGAACCCCTTACGACGAGATGACGACGTTTCTGAAGGCTGACCTGC 976
Db 956 ATATGGGGGCGACCGGACCTTGCAGAGGAAGTGGACACGTTCTCTGAAGCGCGGCTGG 1015
QY 977 TGTGCCAGGGGCCGAGCATGCGCGGCTCCGGGCTCTCGAGGCTATGGCAGAGCTTC 1036
Db 1016 CATGCTCTGCCCGGACTGGGAGCTTACTTCAACGAGCTGCAGGGGATG---CACACC 1072
QY 1037 GGCCTCAGCCTGGAGCGGAACCCCATCTTTTATGGGATCTTTTCTCCAGTGGGAG 1096
Db 1073 TGCAGGACACCTCTCTGGGCAACACACACCTTCTTTGGGGTCTTCAAGCACAGTGGGTG 1132
QY 1097 GAGCTGCCATCTCTGCTGTGTGTGCTTCCGACCCCAAGACATCCGGGCGAGTGTGAATG 1156
Db 1133 ACATGTACCTGTGGGCACTCTGTGATACCACTTGAAGAGATCCAGCGGGTGTGTGAGG 1192
QY 1157 GTCCCTTTAGAGAGCTAAACATGACTGCAACAGGGGAGCTGCTGTCTATGGACACGAGG 1216
Db 1193 GCGCTTAAAGAGTACCATGAGGAGGCCAGAGTGGGACCGCTACACTGACCT---G 1249
QY 1217 TGCCTCAGCCTGGAGATGCTGAGTGCATGCGGCAACATGAAGTCCAGCAGTTTGGAT 1276
Db 1250 TACCAGGCGCTCGGCTGTGCTGTGCTTAAACATGGCATGCGGCGCCACGCTACACCA 1309
QY 1277 CTTCACTCTCCCTGCCAGACCGCTGCTCACCTTTATCAGAGACCACTCTCATGGACA 1336
Db 1310 GCTCCTTGAGCTACCCGCAACATCTCTCAACTCTGCTCAAGAGACCCGCTGTGAGG 1369
QY 1337 GCGCGCTGTCCGCTGACGCGCGCCCTGCTGTCTACTACAGATACAGCCTATCTCA 1396
Db 1370 AGCAGTGGGGCTCGGTGGAGCGCGCCCTGCTGTGAAGAGGGCACCACCTTCAACC 1429
QY 1397 GAGTGTGGCCACAGGTGACCGCTCTCAGGAGGAAGAATATGAGTGTCTTACCTGG 1456
Db 1430 ACCTGTGTGGCCACCGGTTACAGGACTTGATGGAGCCACCTATACAGTGTCTTCAATG 1489
QY 1457 GGACAGAGATGGACACCTCCACCGGCTGTGCGCATTTGGAGCTCAGCTCAGTGTCTGG 1516
Db 1490 GCACAGGAGCGCTGGCTGTCTCAAGGCTGTGAGCCTGGGGCCCTGAGCTGATTTG 1549
QY 1517 AGGATCTGGCCTTGT---CCAGAACACAGCCCGTTGAGAGCATGAATTTGTACCAG 1573
Db 1550 AGGAGTGCAGCTGTTTGACAGGAGGCCATGAGAGCCTGTGTCTATCTCAGAGCAAGA 1609
QY 1574 ATTGGCTCTGTGGGCTCCCATACTGAGGTGACACAGTGAACACCACTGTGGCC 1633
Db 1610 AGCTGCTCTTGGCGGCTCCGCTCTCAGCTGTGAGCTGCGCCGCTGGCCGACTGCATAA 1669
QY 1634 GTCTCCAGAGCTGCTGGAGTGTATCTTGGCCCGAGGACCCGCTGTGGCCTTGAGCTTCC 1693
Db 1670 AGTATCGCTCTGTGAGACTGTGTCTCGCCCGGAGCCCTATTGCGCCTGGAGGCTCA 1729
QY 1694 GCGTTGATCTGTGTGGCCCGCGCGGCA 1724
Db 1730 ACACAGCGCGTGTGTGGCGGTGGTGCCA 1760

RESULT 15
US-10-002-304-13
; Sequence 13, Application US/10002304
; Publication No. US20030036185A1
; GENERAL INFORMATION:
; APPLICANT: Shlmkets, Richard
```

```
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meijia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: Polynucleotides and polypeptides encoded thereby
; FILE REFERENCE: 15966-554 Cura-54 CON-58
; CURRENT APPLICATION NUMBER: US/10/002,304
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 2284
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (166)..(1953)
; NAME/KEY: variation
; LOCATION: (1)..(2284)
; OTHER INFORMATION: N may be any nucleotide
US-10-002-304-13

Query Match 6.2%; Score 248.6; DB 14; Length 2284;
Best Local Similarity 52.1%; Pred. No. 5,5e-58;
Matches 704; Conservative 0; Mismatches 629; Indels 18; Gaps 6;

QY 383 GAAGATCGACTGGATGTGTACCTGAGACTCAGACAGAGAACTGCAGAGAAAGGAAG- 441
Db 419 GAGCATCTCTCTGGGAGGCCCGCTGGAGAAGAAGACTGAGTGTATCCAAAGGAAGA 478
QY 442 --AAGAGACCAATGTACAAATTTATCCAGATTCTCCCATTTGTCATGCTCTCAC 499
Db 479 ACAACGAGACCGAGTGTCTCAACTTCATCCGTTCTCTGAGCCCTTACAATGCTCCACC 538
QY 500 TCCTCAGCTGCGGCGACCTTTCGCTTTTGATCCGAAAGTGGGGGTATTGATGTCTCAGTT 559
Db 539 TGTACGTCTGTGCGACCTTACGCTTCCAGCCCAAGTGCACCTAGCTACATGCTCACCT 598
QY 560 TCCA---GCAGTTTGAAGACTGTGAGAGCGCGCGGGGAAATGTCCTTTTGAGCCAGCTC 616
Db 599 TCACCTTGGAGCATGGAGAGTTTGAAGATGGGAAGGCAAGTGTCCCTATGACCCAGTA 658
QY 617 AACGTCAGCAGCTGTATGCTGGGGGCTCTCTACACCGCCACTGTGAAGAAGTCC 676
Db 659 AGGGCATCTGGCTTCTTGTGGATGGTGTGAGTGTACTCGGCCACACTCAACAATTC 718
QY 677 TGGGACTGAGCCCATCATCTCCGAGCTGTGGGTGAGCTGAGGACTGGATTTCGAACAG 736
Db 719 TGGGCAGCAACCCATATCTCTGCTAATACATGGGG---CCACCACTCCATGAAGACAG 775
QY 737 AGACCTTGTATCTCTGGCTTAATGTCTCAGCCCTTTGTCGAGCTATGTCCTGAGCCAG 796
Db 776 AGTACCTGGCTTTTGGCTCAACGAACTTCTGTTAGGCTCTGCTATGACCTGAGA 835
QY 797 CTGAGTGGGGGATGAAGATGGAGAGTGAAGTAAATCTTTTCTTCTACGAGACCTCC 856
Db 836 GTGTGGGAGCTTACGGGGGAGCAGCAAGTGTACTTCTTCTTCTGAGGAGCGGCAG 895
QY 857 GAGTGTGGACTCTCTATGAGCGCATCAAGGTCCCAAGAGTGGCCCGAGTGTGTGGGGG 916
Db 896 TGGAGTCCGACTGCTATGCGGAGCAGTGTGTGTGGCCCGTGTCTGCAAGGGCG 955
QY 917 ACCTTGGGGGAGGAAGACCTTTCAGCAGAGATGGAGAGCTTTCTGAAGGCTGACCTGC 976
Db 956 ATATGGGGGCGCACGACCCCTGCAGAGGAAGTGGACACGCTTCTCTTGAAGCGCGCTGG 1015
QY 977 TGTGCCAGGGGCCGAGCATGCGCGGCTCTCGGGGTTCTGCAAGGCTATGGCAGCTTC 1036
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Db 1016 CATGCTCTGCCCGCAACTGGAGCTCTACTTCAACAGCTGCAGGCGCATG---CACACCC 1072
Qy 1037 GGCCTAGCCTGGAGCGGGAACCCCATCTTTTATGGATCTTTTCTCCAGTGGGAAG 1096
Db 1073 TGCAGGACACTCTCTGCGACACACACACTTCTTTGGGGTTTTCAGACACAGTGGGGTG 1132
Qy 1097 GAGCTGCCATCTCTGCTGTGTGTGCTTCCGACCCCAAGACATCCGGGGCAGTGTGAATG 1156
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 25, 2003, 19:14:04 ; Search time 8343.28 Seconds
(without alignments)
11429.597 Million cell updates/sec

Title: US-09-284-180a-2

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Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_on.*

21: em_or.*

22: em_ov.*

23: em_pat.*

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25: em_pi.*

26: em_ro.*

27: em_sts.*

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32: em_htg_other.*

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36: em_htg_mam.*

37: em_htg_vit.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2331	100.0	4008	10	AB002563	AB002563 Rattus no
2	2150	92.2	4002	10	AB021291	AB021291 Mus muscu
3	2004	86.0	2354	10	AF038652	AF038652 Mus muscu
4	1827.6	78.4	2948	9	BC038411	BC038411 Homo sapi
5	1827.6	78.4	2971	6	AX136143	AX136143 Sequence
6	1827.6	78.4	2971	6	BD123524	BD123524 Secretary
7	1827.6	78.4	2971	6	AK075384	AK075384 Homo sapi
8	1827.6	78.4	4293	9	HS0801526	AL136552 Homo sapi
9	1626	69.8	2893	6	AX003081	AX003081 Sequence
10	1626	69.8	2893	6	BD177663	BD177663 SBSEMN1 p
11	1626	69.8	2893	6	E35443	E35443 SBSEMN1 pol
12	1626	69.8	2894	6	AX003083	AX003083 Sequence
13	1626	69.8	2894	6	BD177664	BD177664 SBSEMN1 p
14	1626	69.8	2894	6	E35444	E35444 SBSEMN1 pol
15	1441.2	61.8	2672	9	AB021292	AB021292 Homo sapi
16	1190.4	51.1	2507	9	BC018361	BC018361 Homo sapi
17	1188.8	51.0	2400	9	AB022317	AB022317 Homo sapi
18	1023	43.9	1913	9	AF053369	AF053369 Homo sapi
19	654	28.1	799	6	AX003085	AX003085 Sequence
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21	654	28.1	799	6	E35445	E35445 SBSEMN1 pol
22	616.8	26.5	2669	9	AB047604	AB047604 Macaca fa
23	616	26.4	250709	2	AC135520	AC135520 Rattus no
24	569.6	24.4	3205	10	AB022311S6	AB022316 Mus muscu
25	569.6	24.4	109332	2	AC134899	AC134899 Mus muscu
26	569.6	24.4	162691	10	AC003061	AC003061 Mouse Chr
27	569.6	24.4	214837	10	AC007305	AC007305 Mus muscu
28	466.2	20.0	64154	2	AL451003_3	Continuation (4 of
29	466.2	20.0	110000	2	AL451003_2	Continuation (3 of
30	466.2	20.0	126228	9	AC006543	AC006543 Homo sapi
31	466.2	20.0	234523	9	AC006544	AC006544 Homo sapi
32	454.2	19.5	163903	9	AC007387	AC007387 Homo sapi
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35	296	12.7	2406	9	AK095587	AK095587 Homo sapi
36	251.8	10.8	3293	6	AX174731	AX174731 Sequence
37	248.6	10.7	2155	6	AX060303	AX060303 Sequence
38	248.6	10.7	2156	6	AX060313	AX060313 Sequence
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40	248.6	10.7	2646	6	AX0704763	AX0704763 Sequence
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44	247.8	10.6	3112	6	AX528279	AX528279 Sequence
45	247	10.6	3781	6	AX376386	AX376386 Sequence

ALIGNMENTS

RESULT 1

AB002563

LOCUS

DEFINITION

AB002563

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

1 (sites)

REFERENCE

AUTHORS

AB002563 Rattus norvegicus mRNA for semaphorin W, complete cds.
4008 bp mRNA linear ROD 09-APR-1999

AB002563

AB002563.1 GI:4519426

semaphorin W.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

Encinas, J.A., Kikuchi, K., Chedotal, A., de Castro, F., Goodman, C.S.

and Kimura, T.

Cloning, expression, and genetic mapping of Sema W, a member of the semaphorin family
Proc. Natl. Acad. Sci. U.S.A. 96 (5), 2491-2496 (1999)
99162633
10051670
2 (bases 1 to 4008)
Kimura, T. and Kikuchi, K.
Direct Submission
Submitted (31-MAR-1997) Toru Kimura, Sumitomo Pharmaceuticals
Research Center, Discovery Research Laboratories II; 1-98, Kasugade
Naka 3-chome, Konohana-ku, Osaka, Osaka 554, Japan
(E-mail: tkimura@sumitomopharm.co.jp, Tel: 06-466-5228,
Fax: 06-466-5491)

FEATURES SOURCE

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CDS

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1 (sites)			
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AUTHORS			
Encinas, J.A., Kikuchi, K., Chedotal, A., de Castro, F., Goodman, C.S.			
and Kimura, T.			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
REFERENCE			
2 (bases 1 to 4002)			
Encinas, J.A., Hanafusa, H. and Kimura, T.			
Direct Submission			
TITLE			
JOURNAL			
Submitted (16-DEC-1998)			
Research Center: 3-1-98 Kasugade-naka, Konohana, Osaka 554-0022,			
Japan (E-mail:tkimura@sumitomopharm.co.jp, Tel:81-6-6466-5228,			
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RESULT 3

AF038652
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

2354 bp
Mus musculus semaphorin M mRNA, partial cds.
AF038652
AF038652
AF038652.1
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2354)
Jang, W., Spillson, S.V., Hua, A., Roe, B. and Meisler, M.H.

AF038652
Mus musculus semaphorin M mRNA, partial cds.
AF038652
AF038652.1
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2354)
Jang, W., Spillson, S.V., Hua, A., Roe, B. and Meisler, M.H.

TITLE Large-scale comparative sequence analysis of human and mouse
JOURNAL genomic DNA reveals coding regions of three new genes
REFERENCE 2 (bases 1 to 2354)
AUTHORS Jang, W., Spilson, S.V. and Meisler, M.H.
TITLE Direct Submission
JOURNAL Submitted (12-Dec-1997) Human Genetics, University of Michigan,
4708 MS II, Box 0618, Ann Arbor, MI 48109-0618, USA
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RESULT 5
AX136143

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DEFINITION Sequence 65 from Patent EP1067182.
ACCESSION AX136143
VERSION AX136143.1 GI:14272551
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE	1	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
AUTHORS		Secretory protein or membrane protein
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QY	1441	GAGGATCTGGCTTGTTCAGAACACACCGCGGTGTGAGAGCATGAAATTTGACACGAT 1500
DB	1528	GAAGATCTGGCTTATTCAGAGGACACAGCGAGTGGAAATGTAACACAGC 1587
QY	1501	TGGCTCTGGTGGGTCCCATACTGAGGTGACAAAGTGAACACAGCAACTGTGGCGCT 1560
DB	1588	TGGCTCTGGTGGGTCCCGTACTGAGGTGACAAAGTGAATTAACAACTGTGGCGCT 1647
QY	1561	CTCCAGAGCTGCTGGAGTGTATCTGCGCCAGGACCCCGCTGCGCTGAGCTTCCGG 1620
DB	1648	CTCCAGAGCTGCTGAGAGTGTATCTGCGCCAGGACCCAGCTGCTGCTGAGCTTCCGG 1707
QY	1621	CTTGATGCTTGTGTGGCCACCGCGCGGAGCACCGCGGGATGGTTCAAGATATAGATCA 1680

QY	841	GACCTTGGGGGAGGAGAACCCCTTACAGAGAGATGGACGACGTTTCTGTAAGAGCTGACCTG	900
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Db	988	CTGTGCCAGGCGCTGAGCATGGCGGGGCTCCAGTGTCTCCAGGATGTTCTGTGCTT	1047
QY	961	CGGCTCTCAGCTGGAGCGGAACCCCAATCTTTTATGGGATCTTTTCCTCCAGTGGGAA	1020
Db	1048	CGACCTGAGCTTGGGCGAGGACTCCCATCTTTTATGGCATCTTTTCTCCAGTGGGAG	1107
QY	1021	GGAGTGGCCATCTCTGCTGTGTGCTTCCGACCCCAAGACATCCGGGCGAGTGTGTAAT	1080
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QY	1141	GTGCCCGACCCAGACCTGGAGGTGCATCGCAACAACATGAAGCTCCAGCAGTTTGA	1200
Db	1228	GTGCCCGACCCAGACCTGGAGGTGCATCACCACAACATGAAGCTCCGGCAGTTGGC	1287
QY	1201	TGCTCACTCTCCCTGCGCAGACCGGTGTCTACCTTTATCAGAGACACCCCTCTCATGGAC	1260
Db	1288	TCATCTCTCTCCCTGCGCTGACCGCGTACTCACTTCATCCGGGACCAACCCACTCATGGAC	1347
QY	1261	AGGCGCGTGTCCCGGCTACGCGCGCCCGCTGCTGCTCACTACAGATACAGCCATCTC	1320
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Db	1408	AGAGTCTGTGGCCACAGAGGTGACCAAGCTCTCAGGGAAGAAATATGACGTGCTACCTG	1467
QY	1381	GGACAGAGGATGGACACCTCCACCGGGGTGTGGCGATTTGGAGCTCAGCTAGTCTTGTG	1440
Db	1468	GGACAGAGGATGGACACCTCCACCGAGCAGTCCGAGTCCGAGCTCAGCTCAGCGTCTT	1527
QY	1441	GAGGATCTGCCTGTTCACAGACACACAGCGGTGTGAGAGCATGAAATGTACACGAT	1500
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Db	1648	CTCCAGAGCTGTCTAGAGTGCATCTGTGGCCCGAGGACCCAGTGTGTGCTTGGAGCTTC	1707
QY	1621	CTTGATGCTGTGTGCGCCACCGCGGAGCAGCCGGGATGGTTCAGATATAGATCA	1680
Db	1708	CTGGATGAGTGTGTGCGCCATCCGGGGGAGCAGCGAGGTGTGTCAAGACATAGATCA	1767
QY	1681	GCGGATGTCTCTCTTTGTGTCCAAAGAACCTGGAGAACATCCCGTAGTGTTTGAAGTT	1740
Db	1768	GCAGATGTCTCTCTTTGTGTCTTAAGAGCTTGAGAACGTCAGTAGTGTTTGAAGTT	1827
QY	1741	CGGGTGGCTACTGTGGGCGACGTGTCTGTGCCATGTTCCTCCCGAGTTCGTGCTTGGCATCC	1800
Db	1828	CCCGTGGCTACAGCTGCGCATGTGTGTCTTGGCCATGTCTCCAAAGCTCAGCATGGGCATCC	1887
QY	1801	TGTGTGTGCGCACCGCCAGTGGAGTACTGGCTCACTCCCGGAGGATGGACTAGAG	1860
Db	1888	TGTGTGTGCGCACCGCCAGTGGAGTACTGGCTCACTCACTCCCGGAGGATGGACTAGAG	1947
QY	1861	GTGGTGGTGAACCCAGGGGCGCTTATGCTTGGAGTGTGAGGAGGTGGAGCC	1920
Db	1948	GTGGTGGTGAACCCAGGGGCGCTTATGCTTGGAGTGTGAGGAGGTGGGCA	2007
QY	1921	GCCCGGTGGTGGCTGCTTATAGCTTGGTGGGCGAGCCAGCGGGGACCCCTCAAAACCGG	1980
Db	2008	GCCCATGTGGTAGCAGCTTACAGCTTGGTATGGGCGAGCCAGCAGATCTCCGAGCCCG	2067
QY	1981	GCCACACCGTTGTGGGGCTGATTTGGTTGCTTCTCCTGGTCTTCTTCAGCAGATCC	2040
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Db	2125	CTGACTCTCATCTTGTGCTGGCTCAGCAGCGGCGCAGCAGAGGAGAACTTCTGGCT	2184
QY	2101	AGAGACAAGTGGGCTTAGATCTGGGGGCTCCACCTCTTGGGACCAACAGCTATAGCTAG	2160
Db	2185	AGAGACAAGTGGGCTTGGACCTGGGGGCTCCACCTTCTGGGACCAACAGCTATAGCTAG	2244
QY	2161	GACCTCTCCCTCTCCGCTCGGCTCAAGATGAACGCTGCGCCCTGGCTGGTGAAGCGGCG	2220
Db	2245	GACCTCTCCCTCTCCGCTCTCTGAAGATGAGCGGTGCGCCCTGGCTGGCAGAGGCGC	2304
QY	2221	AGTGGTTTTGTGGCTTCCCTCCACCTTCTCTGCTGGATTTGGCCCAAGCCAGCCAC	2280
Db	2305	AGTGGTTTTGTGGATTTCTCACCCCTTCTCTGCTTGTGATCTTGGCCCAAGCCAGCCAC	2364
QY	2281	ATCCGGCTCACTGGGGGCGCTCTAGCCAGCTGTGATGAGACCTCCATCTA	2330
Db	2365	ATTCGGCTAACTGGGGCTCTCTAGCCACATGTGATGAACATCCATCTA	2414
RESULT 7			
AK075384		2971 bp mRNA linear PRI 03-SEP-2002	
LOCUS		Homo sapiens cDNA PSEC0074 fis, clone NT2RP2003050, highly similar to Mus musculus mRNA for semaphorin W.	
DEFINITION			
ACCESSION		AK075384	
VERSION		AK075384.1 GI:22761435	
KEYWORDS		oligo capping; fis (full insert sequence).	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE			
AUTHORS		1 Ota, T., Nishikawa, T., Suzuki, Y., Kawai-Hio, Y., Kawai-Hio, Y., Hayashi, K., Ishii, S., Saiko, K., Yamamoto, J., Wakamatsu, A., Nagai, T., Nakamura, Y., Nagahari, K., Sugano, S., and Isogai, T.	
TITLE		HRI human cDNA sequencing project	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 2971)	
AUTHORS		Isogai, T. and Yamamoto, J.	
TITLE		Direct Submission	
JOURNAL		Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)	
COMMENT		HRI human cDNA sequencing project; cDNA 5' - & 3' - end one pass sequencing, clone selection and full insert sequencing; Helix Research Institute (supported by Japan Key Technology Center etc.); cDNA library construction; Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center.	
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BASE COUNT 582 a 853 c 858 g 678 t
ORIGIN

Query Match 78.4%; Score 1827.6; DB 9; Length 2971;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 2033; Conservative 0; Mismatches 279; Indels 18; Gaps 2;
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DB 103 ATGCGCGGCTCTGCTGCGCGCGCGCGCGCGCGCGCGCGCTACAGCCTCGCCCTTC 162
QY 61 CCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 163 CC-----GCTACTGCTGCTGCGGCTGCTGAGCGCGCGCGGATCGCGCGC 207
QY 121 GTCCCCCGCTCAGTGCCAGAACCTCGCTGCCATCTCCGAGCTCGACTCTATCTCAC 180
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DB 1888 TGTGTGGCCACGCGCAGTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG

DB 808 GCCGAATGGGGGATGAAGATGGAGACGACGAAATCTACTTCTTCTTCTTACGAGACATTC 867
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DB 1888 TGTGTGGCAGCCAGCCAGTGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1947

QY	1861	GTGGTGGTGACCCAGGGGCCATGGGGCTTTATGCTTGGAGTGTCAAGGAGGTGGAGCC	1920
Db	1948	GTGGTGGTGACCCAGGGGCCATGGCGCTTATGCTGTGAATCTCAGGAGGTGGGGCA	2007
QY	1921	GGCCGGGTGGTGGCTTATAGCTTGTGTGGGCGACGACGGGGAGCCCTCAACCGG	1980
Db	2008	GGCCATGTGGTAGCAGCTTACAGCTTGTGTATGGGCGACCGACGAGATGCTCCGAGCGG	2067
QY	1981	GGCCACACGGTGTGGGGCGTGGATTGGTGGCTTTCTCCCTGGGTGTTCTTGCAGCATCC	2040
Db	2068	GGCCACAC---AGTGGGGCGGAGCTGCTGGCTTCTTCTTGGGATTTCTCGCAGCATCC	2124
QY	2041	CTCAGCTCTCCTGATTGGTGGCGGTGACGAGCGTGGCGACAGAGGAGCTTCTAGCT	2100
Db	2125	CTGACTCTCATTTCTGATTGGTGGCGGTGACGAGCGAGCGGACAGAGGAACCTTCTGGCT	2184
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Db	2245	GACCTTCCCTCCCTCTCCTGAAGATGAGCGGTTGGCGCTGGCCCTGGCCAGAGGGC	2304
QY	2221	AGTGGTTTTGGTGGCTTCCCTCCACCCCTTCTGCTGGATTCTTCCCAAGCCAGCCAC	2280
Db	2305	AGTGGCTTTGGTGGATTCTCACACCCCTTCTGCTTGATCTTGCCTCAAGCCAGCCAC	2364
QY	2281	ATCCGGCTCAGTGGGGCGCTCTAGCCACGTGTGATGAGACTCCATCTA	2330
Db	2365	ATTCCGGCTAACTGGGGCTCCTTAGCCACATGTGATGAACATCCATCTA	2414
RESULT 8			
LOCUS	HSMB01526	4293 bp	linear
DEFINITION	Homo sapiens mRNA; cDNA DKFZp761015121 (from clone DKFZp761015121); complete cds.		
ACCESSION	AL136552		
VERSION	AL136552.1	GI:13276610	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 4293)		
TITLE	Pouscka,A., Klein,M., Mewes,H.W., Gassenhuber,J. and Wiemann,S.		
JOURNAL	Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY		
COMMENT	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@kfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp761015121) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/		
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Qy	301	AGACCCCGAAGGATCGACTGGATGGTACCTGAGACTCACAGACAGAACTCGACGAAGAA	360
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Qy	361	GGCAAGAAAGAGGACGAATGTCACAAATTTTATCCAGATCTCGCCATGTGCAATGCCCTCT	420
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Qy	481	AGTTTCCAGCAGGTTGAAGACTTGAGAGCGCGGGGAAATGTCTTTTGAGCCAGCT	540
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Db	536	CAGCGGTACGACGCTGTAAATGGCTGGGGGGTCTCTATGCTGCCACTGTGAAAACTAC	595
Qy	601	CTGGGACTCAGCCCATCATCTCCGAGCTGTGGGTGCGAGCTCAGACNCTGGATTCGACAA	660
Db	596	CTGGGACGAGGACAAATTTATCACAGAGCAGTGGGTGTCGCCGAGGACTGGATTCGGACA	655
Qy	661	GAGACCTTGTCATCCTGGCTTAATGCTCCAGCCTTTGTCGACGCTATGGTCCTGAGGCCA	720
Db	656	GATACCTTGCTTCTCTGGCTGACGCCCGAGCCTTTGTGCGACCGTGGCCTTGAGGCCA	715
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Qy	1021	GGAGCTGCCATCTGCTGTGTGCTTCCGACCCCAAGACATCCGGGAGTCTGTAAT	1080
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[illegible]

RESULT 11
E35443
LOCUS
DEFINITION
ACCESSION

Qy	541	CAACGGTTCAGACGTGTAATAGGCTGGGGGGTCTCTTACACCGCCACTGTGAAGAACTTC	600
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Qy	601	CTGGGGACTGAGCCCATCATCTCCGAGCTGTGGGTGCAGCTGAGNACTGGATTGACACA	660
Db	596	CTGGGGACGAGCCAAATTATCACAGACAGTGGTCTGCCGAGGACTGGATTTCGGACA	655
Qy	661	GAGACCTTGTCATCTCGCTTAATGCTCCAGCCCTTTGTCGACGCTATGGTCCCTGAGCCCA	720
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Db	716	GCCGAATGGGGGATGAAGATGGAGACGAGAAATCTACTTCTTTACGGAGACTTCC	775
Qy	781	CGAGTGTGGACATCTATGAGCGCATCAAGGTCCCAAGAGTGGCCCGAGTGTGTGGGGG	840
Db	776	CGAGCATTTGACTCATACGAGCGCATTTAAAGTCCACGGTGGCCGTGTGTGGGGGG	835
Qy	841	GACCTTGGGGCAGGAAGACCCCTTCAGCAGAGATGGACGACTTCTCTGAAGGCTGACCTG	900
Db	836	GACCTCGGGCGGAAGACCCCTCCAGCAGAGATGACGACGTTTTTGAAGCTGACCTG	895
Qy	901	CTGTGCCACGGGCCGAGCATGCGCGGGCTCCGGGGTCTTCGAGGCTATGGCAGAGCTT	960
Db	896	CTCTGTCCAGGCTTGAGCATGCGCGGGCTCCAGTGTCTCGAGGATGTGCTGTGCTT	955
Qy	961	CGGCTCAGCCTGGAGCGGGAACCCCATCTTTTATGGGATCTTTTCTCCCACTGGGAA	1020
Db	956	CGACCTGAGCTTGGGCAGGAGCTCCCATCTTTATGGCATCTTTCTCCCACTGGGAG	1015
Qy	1021	GGAGTCCCATCTCTGCTGTGTGTGCCCTCCGACCCCAAGACATCCGGGAGTGCTGAAT	1080
Db	1016	GGGGCTACTATCTCTGCTGTGTGCCCTCCGACCAAGACATTCGGACAGTCTGTAAT	1075
Qy	1081	GGTCCCTTTAGAGAGCTAAACATGACTGCAACAGGGGACTGCTGTCTATGGACAAACGAG	1140
Db	1076	GGTCCCTTCAGAGAACTAAAACATGACTGCAACAGAGGACTGCTGTCTGGGACAATGAT	1135
Qy	1141	GTGCCACGCCAGACCTTGAGAGTGCATCGCCCAACACATGAAGCTCCAGCAGTTTGGGA	1200
Db	1136	GTGCCACGCCAGACCTTGAGAGTGCATCACCACAACATGAAGTCCGGCACTTTGGC	1195
Qy	1201	TCCTCACTCTCCCTGCCAGACCGGTGCTCACCTTTATCAGAGACCACTCTCATGGAC	1260
Db	1196	TCATCTCTCTCCCTGACCGGTTACTCACCTTATCCGGGACCACTCATATGGAC	1255
Qy	1261	AGGCCCGTGTCCGGCTGACGGCCGCCCTCTGCTGGTCACTACAGATACAGCTATCTC	1320
Db	1256	AGGCCAGTGTTCAGCTGATGGCCACCCCTCTGCTGCTCACTACAGATACAGCTATCTC	1315
Qy	1321	AGAGTCGTGGCCACAGGGTGACCAAGCTCTCAGGGAAGAATAATGACGTGCTTACCTG	1380
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Qy	1381	GGGACAGAGATGGACACCTCCACCGGGCTGTGCGATTCGAGCTCAGCTCAGTGTCTTG	1440
Db	1376	GGNACAGAGATGGACACCTCCACCGAGCAGTGCAGATCGGAGCTCAGCTCAGCTTCTT	1435
Qy	1441	GAGGATCTGCCCTTGTTCAGAACCAACAGCCGGTTGAGAGCATGAAATGTATACACGAT	1500
Db	1436	GAAGATCTGCCCTTATTTCCAGAGCCACAGCCAGTTGAGAACATGAATTTATACACAGC	1495
Qy	1501	TGGCTCTGTGGGTCCCATACTGAGGTGACACAAGTGAACACAGCAACTGTGGCCGT	1560
Db	1496	TGGCTCTGTGTGGCTCCCTACTGAGGTGACACAAGTGAATACACCACTGTGGCCGT	1555
Qy	1561	CTCCAGAGCTGCTCGGAGTGTATCTTGGCCCGAGCCCGTGTGGCTTGGAGCTTCCCG	1620
Db	1556	CTCCAGAGCTGCTCAGAGTGCATCTTGGCCCGAGCCCGTGTGGCTTGGAGCTTCCCG	1615
Qy	1621	CTTGATGCTGTGTGGCCCAACCGCGGAGCAGCCGGGATGGTTCAAGATATAGAGTCA	1680

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1081	Qy	GGTCCCTTTAGAGAGCTAAACATGACTGCAACAGGGGACTGCGTGTCTGATGGACAACGAG	1140
1076	Db	GGTCCCTTCAGAGAACCTAAACATGACTGCAACAGAGAGACTGCGTGTCTGCGTGGACAATGAT	1135
1141	Qy	GTGCCCCAGCCCCAGACTGTGAGAGTGAATCGCCCAACATGAAGCTTCCAGCAGCTTTTGGA	1200
1136	Db	GTGCCCCAGCCAGACCTTGAGAGTGTGATCACCACAACATGAAGCTCCGGCACCTTTGGC	1195
1201	Qy	TCCTCACTCTCCCTGCCAGACCGCGTCTCACCTTTATCAGAGACCAACCCTCTCATCGAC	1260
1196	Db	TCATCTCTCCCTGCGCTACCGGGTACTCACCTTCATCGGGAGCAACCACCTCATGGAC	1255
1261	Qy	AGGCCCGTGTTCGCGGCTGACGGCGCGCCCTGCTGTGCTCACTACAGATACAGCCTATCTC	1320
1256	Db	AGGCCAGTGTTCAGCTGATGGCCACCCCTGCTGTGCTCACTACAGATACAGCCTATCTC	1315
1321	Qy	AGAGTCGTGGCCCCACAGGGTGACAGGCTCTTCAGGGAAAGAAATATGACGTGCTCTACCTG	1380
1316	Db	AGAGTCGTGGCCCCACAGGGTGACAGGCTCTTCAGGGAAAGAGTATGATGTGCTCTACCTG	1375
1381	Qy	GGGACAGAGATGACACCTCCACCCGGCTGTGCGCATTCGGAGCTCAGCTCAGTGTCTTG	1440
1376	Db	GGGACAGAGATGACACCTCCACCGAGCAGTGGCGATTCGGAGCTCAGCTCAGCGTCTT	1435
1441	Qy	GAGGATCTGGCCTTTGTTCCCAAGAACACAGCCGGTTGAGAGCATGAATTTGACACAGAT	1500
1436	Db	GAAGATCTGGCCTTATTTCCAGAGCCACAGCCAGTTTGAGACATGMAATTTGTACCAACAGC	1495
1501	Qy	TGGTCTCTGTGGGCTCCCATACTGAGGTGACACAAGTGAACACCAAGCAACTGTGGCGGT	1560
1496	Db	TGGTCTCTGTGGTCCCGTACTGAGGTGACACAAGTGAATACAACAACACTGTGGCGGT	1555
1561	Qy	CTCAGAGCTGCTCGGAGTGTATCTCTGGCCCCAGACCCCGTGTGCGCCTGGAGCTTCGG	1620
1556	Db	CTCAGAGCTGCTCAGAGTGCATCTCTGGCCCCAGACCCAGTCTGTGCTGGAGCTTCGG	1615
1621	Qy	CTTGATGCTGTGTGGCCACGCGCGGAGCACCGCGGATGGTTTCAAGATATAGAGTCA	1680
1616	Db	CTGGATGAGTGTGTGGCCCATGCGCGGAGGACCGAGGGTTGGTTCCHAGACATAGAGTCA	1675
1681	Qy	CGGATGTCTCTTCTTTGTGTCCAAAAGAACCTGGAGAACATCCGCTAGTGTGTTTGAAGTT	1740
1676	Db	GCAGATGTCTCTTTTGTGTCTTAAAGAGCCTTGAGAGCCTCGAGAACGTCCAGTAGTGTGTTGAAGTT	1735
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1736	Db	CCCTGGCTACAGCTGCGCATGTGGTCTTGCCATGTTTCCANGCTCAGCATGGGCATCC	1795
1801	Qy	TGTTGTGGACACAGCCAGTGGAGTGACTGCGCTCACTCCCGGGAGGATGGACTAGAG	1860
1796	Db	TGTTGTGGACACAGCCAGTGGAGTGACTGCACTCACCCCCGCGGGATGGACTGGAG	1855
1861	Qy	GTGTTGTGACCCAGGGGCCATGGGGCTTATCTTTGCGAGTGTCAAGAGGGTGGAGCC	1920
1856	Db	GTGTTGTGACCCAGGGGCCATGGGCGCTTATGCTGTGAATCTCAGGAGGGTGGGCA	1915
1921	Qy	GCCCGCGTGGTGGCTGCTTATAGCTTGGTGTGGGGCAGCCAGCGGGGACCTCAAAACGG	1980
1916	Db	GCCCATCTGGTAGCAGCTTACAGTCTGGTATGGGGCAGCCAGCAGAGATGCTCCGAGCGGG	1975
1981	Qy	GCCACACCGTTGTGGGGCTTGAATGTTGGCTTCTCTCTGGGTGTTCTTGTGCAGCATCC	2040
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2033	Db	CTGACTCTCATTTGATTGTTGCGCGTCAGCAGCGACGGCAGACAGAGGAACCTTCTGGCT	2092
2101	Qy	AGACAAAGTGGGCTTAGATCTGGGGGCTCCACCTTCTGGGACCAACAAGCTATAGTCAG	2160
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[illegible]

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Qy	541	CAACGGTCACAGCTGTAATGGCTGGGGGCTCTCTACACGCCCACTGTGAAGACTTC	600
Db	536	CACGGTTCACAGCTGTAATGGCTGGGGGGTCTCTATGCTGCCACTGTGAAGAACTAC	595
Qy	601	CTGGGACTGAGCCCATCATCTCCCGAGCTGTGGGTGCGAGCTGAGGACTGGATTCGAACA	660
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Qy	721	GCTGAGTGGGGGATGAAGATGAGAGCATGAATCTTTTTCACGGAGACTCTCC	780
Db	716	GCCGAATGGGGGATGAAGATGAGAGCGAGCAATCTACTTCTTTACGGAGACTCTC	775
Qy	781	CGAGTGTGTGACTCCTATGAGCGCATCAAGGTCCCAAGAGTGGCCCCAGTGTGTGCGGG	840
Db	776	CGAGCATTTGACTCATACAGAGCGCATTAAGTCCCAGGGTGGCCGTGTGTGCGGG	835
Qy	841	GACCTTGGGGGAGGAAGACCTTTCAGCAGAGATGGAGACGCTTTGTGAAGGCTGACCTG	900
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Db	896	CTGTGCCAGGGCTGAGCATGCGGGCCCTCCAGTGTCTGCAGGATGTGTGTGCTT	955
Qy	961	CGGCTCAGCTGAGCGGGAAACCCCATCTTTTATGGGATCTTTTCTCCCACTGGGAA	1020
Db	956	CGACCTGAGCTGGGCGAGGACTCCCATCTTTTATGGCATCTTTCTCCAGTGGAG	1015
Qy	1021	GGAGCTGCCATCTCTGTGTGTGCTTCCGACCCCAAGACATCCGGGCGAGTGTGTAAT	1080
Db	1016	GGGGCTACTATCTCTGTGTCTGTGCTTCCGACCAACAGACATTCGGACAGTGTGTAAT	1075
Qy	1081	GGTCCCTTTAGAGAGCTAAACATGACTGCAACAGGGGACTGCTGTTCATGGACAAGAG	1140
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Qy	1141	GTGCCCCAGCCAGACCTGGAGAGTGCATGCCAACAACATGAAGCTCCAGCACTTTGGA	1200
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Qy	1201	TCCTCACTCTCCCTGCCAGACCGGTGCTCACCCTTTATCAGAGACCACTCTCATGGAC	1260
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Qy	1261	AGGCCGTGTCCCGGCTGAGCGCGCCCTGCTGTCTACTACAGATACAGCTATCTC	1320
Db	1256	AGGCCAGTGTTCAGCTGATGGCGCCACCCCTGCTGTCTACTACAGATACAGCTATCTC	1315
Qy	1321	AGAGTCTGTGCCCCACAGGGTGACCAGCTCTCAGGGGAAAGAAATGACGTGCTCACTG	1380
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Qy	1381	GGGACAGAGATGACACACTCCACCGGGCTGTGGCAATTTGGAGCTCAGTCACTGTCTTG	1440
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Qy	1441	GAGATCTGCGCTGTGTTCCAGACACACAGCGGTTTCAGAGCATGAATTTGACCAAGAT	1500
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Qy	1561	CTCAGAGCTGCTCGGAGTGTATCTCTGCGCCAGAGACCCCGTGTGCGCTGGAGCTTCCGG	1620
Db	1556	CTCAGAGCTGCTCAGAGTGCATCTTGCCCCAGAGCCCACTGTGCTCGAGCTTCCGG	1615
Qy	1621	CTTTGATGTTGTGTGGCCCCACGCGGAGCACCGGATGTTTCAAGATATAGAGTCA	1680
Db	1616	CTGATGATGTTGTGTGGCCCCATGCGGGGAGCACCGAGGTTGTCCAAGACATAGAGTCA	1675
Qy	1681	CGGATGTCCTCTTTTGTCTCCAAAAGAACCTTGGAGAACATCCCGTAGTGTTTGAAGTT	1740
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Qy	1741	CCGGTGGCTACTGTGGCCACAGTGGTCTCCCATGTTTCCCCCAGTTCCTGCTGGGCATCC	1800
Db	1736	CCGGTGGCTACTGTCGCATGTTGCTTCCCATGTTTCTCAAGCTCAGCATGGGCATCC	1795
Qy	1801	TGTGTGTGGCACCAGCCAGTGGAGTGACCTGCTCTACTCCCGGAGGAGTGAGCTAGAG	1860
Db	1796	TGTGTGTGGCACCAGCCAGTGGAGTGACCTACACCCCGGGGATGAGCTGGAG	1855
Qy	1861	GTGTGTGTGACCCAGGGCCATGGGGCTTATGCTTTCGAGTGTCTCAGGAGGTGGAGCC	1920
Db	1856	GTGTGTGTGACCCAGGGCCATGGGGCTTATGCTTTCGAGTGTCTCAGGAGGTGGAGCC	1915
Qy	1921	GCCGCGTGTGTGGCTGCTTATAGCTTGGTGTGGGACGACGCGGGGACCTCAACCCGG	1980
Db	1916	GCCCATGTGTAGCAGCTTACAGCTTGGTATGGGGCAGCGAGAGATGCTCCGAGCCGG	1975
Qy	1981	GCCACACCGTGTGGGGCTGGATGTTGGCTTCTCTCGTGGTGTCTTTCGAGCATCC	2040
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Qy	2041	CTCACTCTCTCTCTGATTTGGTGCCTCAGCAGCGTCCGCGACAGAGGAGCTTCTAGCT	2100
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Qy	2101	AGAGACAAGTGGGCTTAGATCTGGGGCTCCACCTTCTGGGACCAACAGTATAGTCAG	2160
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Qy	2221	AGTGGTTTGTGGCTTCCCTCCACCTTCTGCTGGATTTCTTGGCCAGCCAGCCAC	2280
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AUTHORS	Encinas,J.A., Kikuchi,K., Chedotal,A., de Castro,F., Goodman,C.S. and Kimura,T.		
TITLE	Cloning, expression, and genetic mapping of Sema W, a member of the semaphorin family		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (5), 2491-2496 (1999)		
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102: /cgn2_6/ptodata/2/pna/US6047_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	4008	100.0	4008	18	US-09-284-180-1 Sequence 1, Appl
2	4008	100.0	4008	18	US-09-284-180A-1 Sequence 1, Appl
3	2331	58.2	2331	18	US-09-284-180-2 Sequence 2, Appl
4	2331	58.2	2331	18	US-09-284-180A-2 Sequence 2, Appl

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5 2138.8 53.4 2334 46 US-10-144-771-19015
6 2138.8 53.4 2334 91 US-60-360-207-19015
7 1919.6 47.9 3641 97 US-10-170-235-32596
8 1875.2 46.8 2971 26 US-09-611-523-65
9 1875.2 46.8 2971 50 US-10-305-278-65
10 1673.6 41.8 2893 16 US-09-160-762-1
11 1673.6 41.8 2893 16 US-09-160-762-1
12 1673.6 41.8 2893 34 US-09-808-665A-1
13 1673.6 41.8 2893 44 US-10-036-657-41
14 1673.6 41.8 2894 16 US-09-160-762-3
15 1673.6 41.8 2894 34 US-09-160-762-3
16 1673.6 41.8 2894 34 US-09-808-665A-3
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18 1404.2 35.0 2315 18 US-09-284-180-4
19 1391.2 34.7 1761 18 US-09-284-180-5
20 1391.2 34.7 1761 47 US-09-284-180A-5
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22 1189.4 29.7 2660 1 PCT-US02-40059-40
23 934.4 23.3 1141 77 US-60-234-446-1497
24 797.6 19.9 1067 23 US-09-533-389-22
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27 654 16.3 799 16 US-09-160-762-5
28 654 16.3 799 34 US-09-808-665A-5
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31 550.2 13.7 753 32 US-09-758-445-213
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40 505.2 12.6 671 2 PCT-US01-16450-353
41 505.2 12.6 671 2 PCT-US01-16450A-353
42 505.2 12.6 671 49 US-10-264-237-353
43 408 10.2 669 26 US-09-611-523-406
44 408 10.2 669 50 US-10-305-278-406
45 373.6 9.3 2406 46 US-10-108-260A-789

ALIGNMENTS

RESULT 1
US-09-284-180-1
; Sequence 1, Application US/09284180
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN W
; FILE REFERENCE: 20-4546P
; CURRENT APPLICATION NUMBER: US/09/284,180
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4008
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(75)
; FEATURE:
; OTHER INFORMATION: Coding region from residue 76 to 2406
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (1)..(3977)
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: (1)..(4008)

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US-09-284-180-1
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 4008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 CCGGTCCTTTCCCTCCCGCGCGCGGTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 181 CCGGTCGTCGGCGCGCGGTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
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QY 301 GATCTGCTCCTCCACACACTTTTACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 360
DB 301 GATCTGCTCCTCCACACACTTTTACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 360
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DB 361 CCCTTCTCTGGGGAAGACCCCGAAGGATCGACTGAGTGGTACCTGAGACTCAGACAGAC 420
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DB 421 AACTCAGAGAAAGGCAAGAGAGACGAATGTCAACAATTTTATCCAGATTTCTCGCC 480
QY 481 ATTGTCAATGCTCTCACCTCCTCACCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 540
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QY 541 GTTATTGATGTCAGCTTTCCAGAGGTTTGAAGACTTGAGAGCGCGCGCGCGCGGGAATGT 600
DB 541 GTTATTGATGTCAGCTTTCCAGAGGTTTGAAGACTTGAGAGCGCGCGCGCGGGAATGT 600
QY 601 CCTTTTGAGCCAGCTCAACGGTCAGCAGCTGTAATGGTGGGGCGTCTCTACACCGCC 660
DB 601 CCTTTTGAGCCAGCTCAACGGTCAGCAGCTGTAATGGTGGGGCGTCTCTACACCGCC 660
QY 661 ACTGTGAAGAACTTCTCTGGGACTGAGCCCATCATCTCCCGAGCTGTGGGTGAGCTGAG 720
DB 661 ACTGTGAAGAACTTCTCTGGGACTGAGCCCATCATCTCCCGAGCTGTGGGTGAGCTGAG 720
QY 721 GACTGGATTGAGAGAGACCTTTGTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 721 GACTGGATTGAGAGAGACCTTTGTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 781 ATGTCCTGAGCCAGCTGAGTGGGGGATGAAGATGAGACGATGAATCTTTTTC 840
DB 781 ATGTCCTGAGCCAGCTGAGTGGGGGATGAAGATGAGACGATGAATCTTTTTC 840
QY 841 TTCACGAGACCTCCCGAGTGTGGACTCCTATAGCGCATCAAGGTCCCAAGAGTGGCC 900
DB 841 TTCACGAGACCTCCCGAGTGTGGACTCCTATAGCGCATCAAGGTCCCAAGAGTGGCC 900
QY 901 CGAGTGTGTGGGGGACCTTGGGGGAGAGACCTTTCACACAGATGGACGAGTTT 960
DB 901 CGAGTGTGTGGGGGACCTTGGGGGAGAGACCTTTCACACAGATGGACGAGTTT 960
QY 961 CTGAAGGCTGACCTGCTGTGCCAGGGCCGAGCATGGCGGGCTCTCGAG 1020
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Qy	1021	GCTATGCAGAGCTTCGGCCTCAGCCTGGAGCGGGAAACCCCCATCTCTTTTATGGAGTCTTT	1080
Db	1021		
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Db	1081		
Qy	1141	CGGSCAGTGTGAATGGTCCCTTTAGAGAGCTAAACATGACTGCAACAGGGGACTGCGCT	1200
Db	1141		
Qy	1201	GTCATGACAACAGAGTGCOCACAGACCTGGAGAGTGCATCGCCAAACACATGAAG	1260
Db	1201		
Qy	1261	CTCCAGCAGTTTGGATCCTCACCTCCCTGCCAGACCGCGTGTCACTTTTATCAGAGAC	1320
Db	1261		
Qy	1321	CACCTCTCATGACAGCGCCGTTGCCGGCTGAOGGCCGCCCTGTGTCACCTACA	1380
Db	1321		
Qy	1381	GATACAGCCTATCTCAGAGTCTGGGCCACAGGGTGACCAGCCTCTCAGGGAAGAATAT	1440
Db	1381		
Qy	1441	GACGTGCTTACCTGGGACAGAGATGGACACTCCACCGGGTGTGCCATTGGAGCT	1500
Db	1441		
Qy	1501	CAGCTAGTGTCTGGAGGATCTGGCCTTGTTCACAGAACACAGCGGTTGAGAGCATG	1560
Db	1501		
Qy	1561	AAATTGTACCAGATTGCGTCTGGTGGGCTCCCATCTCAGGTGACACAAGTGAACACC	1620
Db	1561		
Qy	1621	AGCAACTGTGGCGTCTCCAGAGCTGCTCGAGTGTATCTTGCGCCACGAGACCCGTGTC	1680
Db	1621		
Qy	1681	GCCTGGAGCTTCGGCTTGATGCTTGTGTGGCCACGCCGGGAGACACC CGGTGCTG	1740
Db	1681		
Qy	1741	CAAGATATAGAGTCAGCGGATGTCTCTCTTTGTGTCAAAAGAACTGAGAACATCCC	1800
Db	1741		
Qy	1801	GTAGTGTTTGAAAGTTCCGGTGGCTACTGTGGGCCACGTGCTCTGCCATGTTCCCCAGT	1860
Db	1801		
Qy	1861	TC TGCCCTGGGCATCTCTGTGTGGCACACGCCAGTGGAGTGACTGGCTACTCCCGG	1920
Db	1861		
Qy	1921	AGGATGGACTAGAGTGGTGGTGACCCACAGGGGCCATGGGGCTATGCTTCGAGTGT	1980
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Db	1981		
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Db	2041		

[illegible]

Qy	781	ATGGTCTCTGAGCCAGCTGAGTGGGGGATGAAGATGGAGACGATGAATCTTTTTTTC	840	1861	TCCTCCCTGGGCATCTGTGTGTGGCACAGCCAGTGGAGTGGCTGCTCACTCCCGG	1920
Dd				Dd		
Qy	781	ATGGTCTCTGAGCCAGCTGAGTGGGGGATGAAGATGGAGACGATGAATCTTTTTTTC	840	1861	TCCTCCCTGGGCATCTGTGTGTGGCACAGCCAGTGGAGTGGCTGCTCACTCCCGG	1920
Dd				Dd		
Qy	841	TTACAGGAGACCTCCCGAGTGTGGACTCTCTATGAGCGCATCAAGGTGCCAAGAGTGGCC	900	1921	AGGATGGACTAGAGTGGTGGTACCACAGGGGCCATGGGGCTTATGCTTGGAGTGT	1980
Dd				Dd		
Qy	841	TTACAGGAGACCTCCCGAGTGTGGACTCTCTATGAGCGCATCAAGGTGCCAAGAGTGGCC	900	1921	AGGATGGACTAGAGTGGTGGTACCACAGGGGCCATGGGGCTTATGCTTGGAGTGT	1980
Dd				Dd		
Qy	901	CGAGTGTGTGGGGGACCTTTGGGGCAGGAAGACCTTCACAGAGATGACACACGTTT	960	1981	CAGGAGGTGGAGCGCCCGCTGCTTATAGCTTGTGTGGGCGAGCAGCAGGG	2040
Dd				Dd		
Qy	901	CGAGTGTGTGGGGGACCTTTGGGGCAGGAAGACCTTCACAGAGATGACACACGTTT	960	1981	CAGGAGGTGGAGCGCCCGCTGCTTATAGCTTGTGTGGGCGAGCAGCAGGG	2040
Dd				Dd		
Qy	961	CTGAAGCTGACCTGTGTGCCAGAGCCCGAGCATGGCGGGCTCCGGGGTCTGCGAG	1020	2041	GGACCTCAAAACCGGGGCCACACCGTTGTGGGGCTGGATTTGCTTCTCTGGGT	2100
Dd				Dd		
Qy	961	CTGAAGCTGACCTGTGTGCCAGAGCCCGAGCATGGCGGGCTCCGGGGTCTGCGAG	1020	2041	GGACCTCAAAACCGGGGCCACACCGTTGTGGGGCTGGATTTGCTTCTCTGGGT	2100
Dd				Dd		
Qy	1021	GCTATGGCAGAGCTTGGGCTCAGCCTGGAGCGGGAACCCCATCTTTATGGATCTTT	1080	2101	GTTCCTTGACGATCCCTCACTCTCTCTGATTTGGTGGCGCTCAGCAGCGTGGCGGACAG	2160
Dd				Dd		
Qy	1021	GCTATGGCAGAGCTTGGGCTCAGCCTGGAGCGGGAACCCCATCTTTATGGATCTTT	1080	2101	GTTCCTTGACGATCCCTCACTCTCTCTGATTTGGTGGCGCTCAGCAGCGTGGCGGACAG	2160
Dd				Dd		
Qy	1081	TCCTCCAGTGGGAAGAGCTGCCATCTCTGTGTGTGCTTCCGACCCCAAGACATC	1140	2161	AGGAGCTTCTAGCTAGACAAAGTGGCTTAGATCTGGGGGCTCCACCTTCTTGGGACC	2220
Dd				Dd		
Qy	1081	TCCTCCAGTGGGAAGAGCTGCCATCTCTGTGTGTGCTTCCGACCCCAAGACATC	1140	2161	AGGAGCTTCTAGCTAGACAAAGTGGCTTAGATCTGGGGGCTCCACCTTCTTGGGACC	2220
Dd				Dd		
Qy	1141	CGGCGAGTGTGAATGTGCCCTTTAGAGAGCTAAACATGACTGCAACAGGGGACTGCCT	1200	2221	ACAAAGCTATAGTACGAGACCTCCCTCTCTCGCTTGAAGATGAACGGCTGCCCTTGCC	2280
Dd				Dd		
Qy	1141	CGGCGAGTGTGAATGTGCCCTTTAGAGAGCTAAACATGACTGCAACAGGGGACTGCCT	1200	2221	ACAAAGCTATAGTACGAGACCTCCCTCTCTCGCTTGAAGATGAACGGCTGCCCTTGCC	2280
Dd				Dd		
Qy	1201	GTATGACACAGAGGTGCCCCAGCCAGACCTGGAGAGTGCATCGCCCAACATGAAG	1260	2281	CTGGGTAAAGCGGGGACGTGGTTTGGTGGCTTCCCTCCACCTTCTCTGGATTTCTTGC	2340
Dd				Dd		
Qy	1201	GTATGACACAGAGGTGCCCCAGCCAGACCTGGAGAGTGCATCGCCCAACATGAAG	1260	2281	CTGGGTAAAGCGGGGACGTGGTTTGGTGGCTTCCCTCCACCTTCTCTGGATTTCTTGC	2340
Dd				Dd		
Qy	1261	CTCCAGCAGTTTGGATCTCACTCTCCCTGCCAGACCGCGTCACTTTATCAGAGAC	1320	2341	CCAAAGCCAGCCACATCCGGCTCACTGGGGGCTCTTAGCCAGGTGTGATGAGACCTTCC	2400
Dd				Dd		
Qy	1261	CTCCAGCAGTTTGGATCTCACTCTCCCTGCCAGACCGCGTCACTTTATCAGAGAC	1320	2341	CCAAAGCCAGCCACATCCGGCTCACTGGGGGCTCTTAGCCAGGTGTGATGAGACCTTCC	2400
Dd				Dd		
Qy	1321	CACCTCTCATGAGACGCGCTGTCCCGGCTGACGGCGCCCGCTGCTGGTCACTACA	1380	2401	ATCTAAAGCCGGGAAATAGACTGCCAGCCATGAGCAGTCTCTGGAACCTAGTGGCTACCA	2460
Dd				Dd		
Qy	1321	CACCTCTCATGAGACGCGCTGTCCCGGCTGACGGCGCCCGCTGCTGGTCACTACA	1380	2401	ATCTAAAGCCGGGAAATAGACTGCCAGCCATGAGCAGTCTCTGGAACCTAGTGGCTACCA	2460
Dd				Dd		
Qy	1381	GATACAGCTATCTCAGAGTCTGGCCACAGAGGTGACACGCTCTCAGGGAAGAATAT	1440	2461	AGACCATGATCATGGCTGCTCTTCTCTGGAGTCTGTGTTCACACATTAGTGTCTG	2520
Dd				Dd		
Qy	1381	GATACAGCTATCTCAGAGTCTGGCCACAGAGGTGACACGCTCTCAGGGAAGAATAT	1440	2461	AGACCATGATCATGGCTGCTCTTCTCTGGAGTCTGTGTTCACACATTAGTGTCTG	2520
Dd				Dd		
Qy	1441	GACGTGCTTACCTGGGACAGAGATGGACACCTCCACCGGGTGTGCGCATTTGGAGCT	1500	2521	TCCTCTGACCTGGACCTGGCTTTTGGCCAGATCTCTGATTTCTCATGAGATCAACCT	2580
Dd				Dd		
Qy	1441	GACGTGCTTACCTGGGACAGAGATGGACACCTCCACCGGGTGTGCGCATTTGGAGCT	1500	2521	TCCTCTGACCTGGACCTGGCTTTTGGCCAGATCTCTGATTTCTCATGAGATCAACCT	2580
Dd				Dd		
Qy	1501	CAGTCTAGTGTCTGGAGGATCTGGCCTTTGCCAGAACACACAGCCGGTTGAGAGCATG	1560	2581	GTAACTTCTCGGATGGCTCTTGTCTTGGGCCATCAGCTTGTGGGTGGAGTAAGGAC	2640
Dd				Dd		
Qy	1501	CAGTCTAGTGTCTGGAGGATCTGGCCTTTGCCAGAACACACAGCCGGTTGAGAGCATG	1560	2581	GTAACTTCTCGGATGGCTCTTGTCTTGGGCCATCAGCTTGTGGGTGGAGTAAGGAC	2640
Dd				Dd		
Qy	1561	AAATTTACACAGATTTGGTCTGGTGGCTCCATCTAGTGGTACACAGTGAACACC	1620	2641	ATAGCCCCGGAAGGGAATCAGTGTGGAGTGTGGGGCTGTGTGCCCTGGCTCTT	2700
Dd				Dd		
Qy	1561	AAATTTACACAGATTTGGTCTGGTGGCTCCATCTAGTGGTACACAGTGAACACC	1620	2641	ATAGCCCCGGAAGGGAATCAGTGTGGAGTGTGGGGCTGTGTGCCCTGGCTCTT	2700
Dd				Dd		
Qy	1621	AGCAACTGTGGCGCTCTCAGAGTGTCTGAGTGTATCTTGGCCAGGACCCCGTGTGC	1680	2701	GTGTGGCTGTATGATTTCCAGTCTGCTGACTCTGGGAGCGCATGATCCCTGACTGC	2760
Dd				Dd		
Qy	1621	AGCAACTGTGGCGCTCTCAGAGTGTCTGAGTGTATCTTGGCCAGGACCCCGTGTGC	1680	2701	GTGTGGCTGTATGATTTCCAGTCTGCTGACTCTGGGAGCGCATGATCCCTGACTGC	2760
Dd				Dd		
Qy	1681	GCCTGGAGCTTCCGGCTTGTGTGTGTGGCCACCGCGCGAGCAGCCCGGGATGGTT	1740	2761	CTTGAGATCTCTCCCACTAGTTTCCCTTGTCTCTGGAAGAGTGTGTCTATACACTG	2820
Dd				Dd		
Qy	1681	GCCTGGAGCTTCCGGCTTGTGTGTGTGGCCACCGCGCGAGCAGCCCGGGATGGTT	1740	2761	CTTGAGATCTCTCCCACTAGTTTCCCTTGTCTCTGGAAGAGTGTGTCTATACACTG	2820
Dd				Dd		
Qy	1741	CAAGATATAGAGTACAGGGATGTCTCTTTGTGTGTCCAAAGAACCTGGAGACATCCC	1800	2821	GTGTGGCTTAGAAGGCTCTCCATGTGTGATTTGGAGCAGAGGCGCGGTGCCCTGGT	2880
Dd				Dd		
Qy	1741	CAAGATATAGAGTACAGGGATGTCTCTTTGTGTGTCCAAAGAACCTGGAGACATCCC	1800	2821	GTGTGGCTTAGAAGGCTCTCCATGTGTGATTTGGAGCAGAGGCGCGGTGCCCTGGT	2880
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Qy	1801	GTAGTGTGTGAAGTTCCGGTGGCTACTGTGGGCGACGTTGCTTCCGATGTTCCCGCAGT	1860	2881	TGGGAGTCGGAGAGAAAAGTTGGAATGGGGGACAACTTAACCTTCGGTAGCAGTGAGG	2940
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Qy	1801	GTAGTGTGTGAAGTTCCGGTGGCTACTGTGGGCGACGTTGCTTCCGATGTTCCCGCAGT	1860	2881	TGGGAGTCGGAGAGAAAAGTTGGAATGGGGGACAACTTAACCTTCGGTAGCAGTGAGG	2940
Dd				Dd		
Qy	1801	GTAGTGTGTGAAGTTCCGGTGGCTACTGTGGGCGACGTTGCTTCCGATGTTCCCGCAGT	1860	2941	GAACACATGCCGTGCCCATCACCACAGCGCTTCTTTAACTTTGAGCAAAAGTTCCC	3000
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[illegible]

RESULT 3

US-09-284-180-2
; Sequence 2, Application US/09284180
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru
; APPLICANT: KIKUCHI, Kaoru
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN W
; FILE REFERENCE: 20-4546P
; CURRENT APPLICATION NUMBER: US/09/284,180
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2331
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Coding region from residue 1 to 2331
US-09-284-180-2

	Query Match	58.2%	Score 2331;	DB 18;	Length 2331;
	Best Local Similarity	100.0%;	Pred. No. 4.9e-307;	Mismatches 0;	Indels 0;
	Matches 2331;	Conservative 0;			Gaps 0;
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Db	1	ATGCTTTGCCAGGGCCGAGCGGGCCCCCGCGGGCCCCCGGGCCCCCGGGTCTTCCTTC	60		
Qy	136	CCGCGCGCGGTGCTGCTGCCTGCTGCTGCTGGCGCATACTAAGCGCCCCGGTGTCGGCGCCG	195		
Db	61	CCGCGCGCGGTGCTGCTGCCTGCTGCTGGCGCATACTAAGCGCCCCGGTGTCGGCGCCG	120		
Qy	196	GTCCCCCGCTCAGTGC GCCAGAACCTCGCTGCCCATCTCCGAGGCTGACCTCTATCTCAC	255		
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Qy	256	CGGTTTGACGCGTCTCATAGTAACAATTACTCTGCTCTCTCTGTGGATCCTGCCTCCCAC	315		
Db	181	CGGTTTGACGCGTCTCATAGTAACAATTACTCTGCTCTCTCTGTGGATCCTGCCTCCCAC	240		
Qy	316	ACACTTTACGTGCGTGCACGGGATGACATCTTCGCTTTAAACCCTCCCTCTCTCTGGGAA	375		
Db	241	ACACTTTACGTGCGTGCACGGGATGACATCTTCGCTTTAAACCCTCCCTCTCTCTGGGAA	300		
Qy	376	AGACCCCGAAGGATCGACTGGATGGTAGCTGACCTGAGACTCACAGACAGAACTGCAGGAAGAAA	435		
Db	301	AGACCCCGAAGGATCGACTGGATGGTAGCTGACCTGAGACTCACAGACAGAACTGCAGGAAGAAA	360		
Qy	436	GGCAAGAAGAGGACGAATGTCAAAATTTATCCAGATTCTCGCCATGTGCAATGCCTCT	495		
Db	361	GGCAAGAAGAGGACGAATGTCAAAATTTATCCAGATTCTCGCCATGTGCAATGCCTCT	420		
Qy	496	CACCTCTCACGTGCGGACCTTCGCTTTTGATCCGAAGTGGGGGTTATGATGTGTCC	555		
Db	421	CACCTCTCACGTGCGGACCTTCGCTTTTGATCCGAAGTGGGGGTTATGATGTGTCC	480		
Qy	556	AGTTTTCCAGCAGGTTGAAAGACTTGAGAGCGGCGGGGAAATGTCTTTTGAGCCAGCT	615		
Db	481	AGTTTTCCAGCAGGTTGAAAGACTTGAGAGCGGCGGGGAAATGTCTTTTGAGCCAGCT	540		
Qy	616	CAACGGTTCAGCAGCTGTAATGGCTGGGGCGGCTCTACACGCCCATCTGTAAGAACTTC	675		
Db	541	CAACGGTTCAGCAGCTGTAATGGCTGGGGCGGCTCTACACGCCCATCTGTAAGAACTTC	600		
Qy	676	CTGGGAGACTGAGCCCATCATCTCCCGAGCTGTGGGTCGAGCTGAGGACTGGATTGCAACA	735		
Db	601	CTGGGAGACTGAGCCCATCATCTCCCGAGCTGTGGGTCGAGCTGAGGACTGGATTGCAACA	660		
Qy	736	GAGACCTTGTCTCTCTGGCTTAATGCTCCAGCCTTTGTGCGAGCTATGCTCTGAGCCCA	795		
Db	661	GAGACCTTGTCTCTCTGGCTTAATGCTCCAGCCTTTGTGCGAGCTATGCTCTGAGCCCA	720		
Qy	796	GCTAGTGGGGGATGAAGATGGAGACGATGAATCTTTTTTTCTTCTACGGAGACCTCC	855		

Db		721	GCTGAGTGGGGGATGAAGATGGAGACGATGAAATCTTTTTTTCTTCACCGGAGACCTCC	780
Qy		856	CGAGTGTGGACTCCTATGACGCATCAAGTGCCAAGAGTGGCCCCAGTGTGTGCGGGG	915
Db		781	CGAGTGTGGACTCCTATGACGCATCAAGTCCCAGAGTGGCCCCAGTGTGTGCGGGG	840
Qy		916	GACCTTGGGGCAGGAAGACCCTTCAGCAGATGGACAGCTTTCTGAAAGGCTGACCTG	975
Db		841	GACCTTGGGGCAGGAAGACCCTTCAGCAGATGGACAGCTTTCTGAAAGGCTGACCTG	900
Qy		976	CTGTGCCACGGCCGAGCATGCGCGGCCTCGGGGTTCTGCAGGCTATGGCAGAGCTT	1035
Db		901	CTGTGCCACGGCCGAGCATGCGCGGCCTCGGGGTTCTGCAGGCTATGGCAGAGCTT	960
Qy		1036	CGGCTCAGCTGGAGCGGAACCCCATCTTTATGGGATCTTTTCTCCCACTGGGAA	1095
Db		961	CGGCTCAGCTGGAGCGGAACCCCATCTTTATGGGATCTTTTCTCCCACTGGGAA	1020
Qy		1096	GGAGCTGCCATCTCTGTGTGTGTGTGTCCGACCCCAAGACATPCGGGCGAGTGCCTGAAT	1155
Db		1021	GGAGCTGCCATCTCTGTGTGTGTGTGTCCGACCCCAAGACATPCGGGCGAGTGCCTGAAT	1080
Qy		1156	GGTCCCTTTAGAGAGCTAAAACATGACTGCGAACAGGGGACTGCCCTGTATGGACAACGAG	1215
Db		1081	GGTCCCTTTAGAGAGCTAAAACATGACTGCGAACAGGGGACTGCCCTGTATGGACAACGAG	1140
Qy		1216	GTGCCCCAGCCAGACCTGGAGAGTGCATCGCAACAACTGAAGCTCCAGCAGTTTGGGA	1275
Db		1141	GTGCCCCAGCCAGACCTGGAGAGTGCATCGCAACAACTGAAGCTCCAGCAGTTTGGGA	1200
Qy		1276	TCTCTACTCTCCCTGCCAGACCGCGTCTCACCTTTATCAGAGACCAACCCTCTCATGGAC	1335
Db		1201	TCTCTACTCTCCCTGCCAGACCGCGTCTCACCTTTATCAGAGACCAACCCTCTCATGGAC	1260
Qy		1336	AGSCCGTGTTCGGGCTGACGGCGGCCCTCGTGTCTACTACAGATACAGCCTATCTC	1395
Db		1261	AGSCCGTGTTCGGGCTGACGGCGGCCCTCGTGTCTACTACAGATACAGCCTATCTC	1320
Qy		1396	AGAGTCTGTGCCACAGGGTGACAGCCTCTCAGGGAAAGAATAATGACGTCTACCTG	1455
Db		1321	AGAGTCTGTGCCACAGGGTGACAGCCTCTCAGGGAAAGAATAATGACGTCTACCTG	1380
Qy		1456	GGACAGAGGATGGACACCTCCACCGGGCTGTGCGCATTTGGAGCTCAGCTCAGTGTCTTG	1515
Db		1381	GGACAGAGGATGGACACCTCCACCGGGCTGTGCGCATTTGGAGCTCAGCTCAGTGTCTTG	1440
Qy		1516	GAGGATCTGCCCTGTTCACAGAACACACCGCGTTGAGAGCATGAAATTGTACCAAGAT	1575
Db		1441	GAGGATCTGCCCTGTTCACAGAACACACCGCGTTGAGAGCATGAAATTGTACCAAGAT	1500
Qy		1576	TGGCTCTGTGGCTCCCATCTGAGGTGACACACAGTGAACACCACTGTGGCCGT	1635
Db		1501	TGGCTCTGTGGCTCCCATCTGAGGTGACACACAGTGAACACCACTGTGGCCGT	1560
Qy		1636	CTCCAGAGCTGCTCGGAGTGTATCCTTGGCCCCAGGACCCCTGTGCGCTCGAGCTTCGGG	1695
Db		1561	CTCCAGAGCTGCTCGGAGTGTATCCTTGGCCCCAGGACCCCTGTGCGCTCGAGCTTCGGG	1620
Qy		1696	CTTGATGCTTGTGTGGCCACAGCGCGGAGACACCGGGGATGTTCAAGATATAGAGTCA	1755
Db		1621	CTTGATGCTTGTGTGGCCACAGCGCGGAGACACCGGGGATGTTCAAGATATAGAGTCA	1680
Qy		1756	GCGGATGCTCTCTTTGTCTCAAAGAACCTGGAGAACATCCCGTAGTGTITGAGTT	1815
Db		1681	GCGGATGCTCTCTTTGTCTCAAAGAACCTGGAGAACATCCCGTAGTGTITGAGTT	1740
Qy		1816	CCGGTGCTACTGTGGGCCACGTGGTCTGCCATGTTCCGCCAGTTCTGCTGGGATCC	1875
Db		1741	CCGGTGCTACTGTGGGCCACGTGGTCTGCCATGTTCCGCCAGTTCTGCTGGGATCC	1800
Qy		1876	TGTGTGGCACCAAGCCAGTGGAGTGACTGCGCTCACCTCCCGGAGGATGACATAGAG	1935
Db		1801	TGTGTGGCACCAAGCCAGTGGAGTGACTGCGCTCACCTCCCGGAGGATGACATAGAG	1860

Qy	1936	GTGTGGTGACCCACGAGGGCCATTATCGTTCGAGTGTCTACGAGGGTGGAGCC	1995
Db	1861	GTGTGGTGACCCACGAGGGCCATTATCGTTCGAGTGTCTACGAGGGTGGAGCC	1920
Qy	1996	GCCCGCGTGGTGCTTATAGCTTGGTGGGACGACAGCGGGACCCCTCAACCGG	2055
Db	1921	GCCCGCGTGGTGCTTATAGCTTGGTGGGACGACAGCGGGACCCCTCAACCGG	1980
Qy	2056	GCCACACCGTGTGGGGGCTGGATGGTTGGCTTCTCCTGGGTCTTGTGCAGCATCC	2115
Db	1981	GCCACACCGTGTGGGGGCTGGATGGTTGGCTTCTCCTGGGTCTTGTGCAGCATCC	2040
Qy	2116	CTCACTCTCCCTGATTGGTGC CGCTCAGACGCTCGGCACAGAGGGAGCTTCTAGCT	2175
Db	2041	CTCACTCTCCCTGATTGGTGC CGCTCAGACGCTCGGCACAGAGGGAGCTTCTAGCT	2100
Qy	2176	AGACACAAGGTGGCTTAGATCTGGGGGCTCCACCTTCTGGGACCAAGCATATAGTCAG	2235
Db	2101	AGACACAAGGTGGCTTAGATCTGGGGGCTCCACCTTCTGGGACCAAGCATATAGTCAG	2160
Qy	2236	GACCTTCGCTCTCCTTGGCCTGAAGATGAACGGCTGCCCTGGCCCTGGGTAAAGCGGGG	2295
Db	2161	GACCTTCGCTCTCCTTGGCCTGAAGATGAACGGCTGCCCTGGCCCTGGGTAAAGCGGGG	2220
Qy	2296	AGTGGTTTTGGTGGCTTCCCTCCACCCCTCTCGCTGGATTTCTTGGCCAAAGCCAGCCAC	2355
Db	2221	AGTGGTTTTGGTGGCTTCCCTCCACCCCTCTCGCTGGATTTCTTGGCCAAAGCCAGCCAC	2280
Qy	2356	ATCCGGGTCTACTGGGGGCGCTCTTAGCCACGTTGTGATGAGACCTCCATCTAA	2406
Db	2281	ATCCGGGTCTACTGGGGGCGCTCTTAGCCACGTTGTGATGAGACCTCCATCTAA	2331

RESULT 4

```

US-09-284-180A-2
; Sequence 2, Application US/09284180A
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru
; APPLICANT: KIMURA, Kaoru
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN W
; FILE REFERENCE: 0020-4546P
; CURRENT APPLICATION NUMBER: US/09/284,180A
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2331
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc:feature
; LOCATION: (1)..(2331)
; OTHER INFORMATION: Coding region
; FEATURE:
; NAME/KEY: misc:feature
; LOCATION: (1)..(2331)
; OTHER INFORMATION: strandedness: double
US-09-284-180A-2

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	Query Match	58.2%	Score 2331;	DB 18;	Length 2331;	
	Best Local Similarity	100.0%;	Pred. No. 4.9e-307;			
	Matches 2331;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0	
Qy	76	ATGCTTGCCAGGGCGGACGGCGCGCGCGGGCGCCCCCGCGCCCTCCGGCTCTTTCCCTTC	135			
Db	1	ATGCTTGCCAGGGCGGACGGCGCGCGCGGGCGCCCCCGCGCCCTCCGGCTCTTTCCCTTC	60			
Qy	136	CCGCGCGCGCTGTGCTGCTGCTGTGCGGATACCTAAGCGCCCGCGGTGCGCGCGCG	195			
Db	61	CCGCGCGCGCTGTGCTGCTGCTGTGCGGATACCTAAGCGCCCGCGGTGCGCGCGCG	120			
Qy	196	GTCCCCCGCTCAGTGCCCGAGAACCTCGCTGCGCCATCTCCGAGGCTGACTCTATCTACCC	255			

Db 121 GTCCCCGCTCAGTGGCCGAACCTCGCTGCCATCTCCGAGGCTGACTCCTATCTCAC 180
QY 256 CGGTTTGCAGCGTCTCATAGTACAATTAAGTCTGCTCTCTCTGTGATCTGCTGCCAC 315
Db 181 CGGTTTGCAGCGTCTCATAGTACAATTAAGTCTGCTCTCTCTGTGATCTGCTGCCAC 240
QY 316 AACTTTACGTCGGTGACGGGATAGATCTTCGCTTTAACCTCCCTCTCTCTGCGGAA 375
Db 241 AACTTTACGTCGGTGACGGGATAGATCTTCGCTTTAACCTCCCTCTCTCTGCGGAA 300
QY 376 AGACCCGGAAGGATCGACTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 435
Db 301 AGACCCGGAAGGATCGACTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 436 GGAAGAAAGAGGACGAATGTCACAAATTTATCCAGATCTCCGCAATTTGCAATGCTCT 495
Db 361 GGAAGAAAGAGGACGAATGTCACAAATTTATCCAGATCTCCGCAATTTGCAATGCTCT 420
QY 496 CACTCTCAGTGGCGCACTTCGCTTTTATCCGAAATGCGGATGCGGATGATGATGATGAT 555
Db 421 CACTCTCAGTGGCGCACTTCGCTTTTATCCGAAATGCGGATGCGGATGATGATGATGAT 480
QY 556 AGTTTCCAGCAGGTTGAAAGACTTGAGAGCGCGCGGGAATGTCCTTTGAGCCAGCT 615
Db 481 AGTTTCCAGCAGGTTGAAAGACTTGAGAGCGCGCGGGAATGTCCTTTGAGCCAGCT 540
QY 616 CAACGGTACGACGCTGAATGCTGGGGGCGTCTCTACACCGCCACTGTGAAGAACTTC 675
Db 541 CAACGGTACGACGCTGAATGCTGGGGGCGTCTCTACACCGCCACTGTGAAGAACTTC 600
QY 676 CTGGGACGTAGCCCAATCATCTCCAGCTGTGGGTCGAGCTGAGGACTGGATTCGAACA 735
Db 601 CTGGGACGTAGCCCAATCATCTCCAGCTGTGGGTCGAGCTGAGGACTGGATTCGAACA 660
QY 736 GAGACCTTGTATCTGGCTTAATGCTCCAGCTTTGTCGAGCTATGCTGAGCCCA 795
Db 661 GAGACCTTGTATCTGGCTTAATGCTCCAGCTTTGTCGAGCTATGCTGAGCCCA 720
QY 796 GCTGAGTGGGGGATGAAGATGGAGACGATGAATCTTTTTCACGGAGACCTCC 855
Db 721 GCTGAGTGGGGGATGAAGATGGAGACGATGAATCTTTTTCACGGAGACCTCC 780
QY 856 CGAGCTTGGACTCCTATGAGCGCATCAAGTCCCAAGAGTGGCCGAGTGTGGGGG 915
Db 781 CGAGCTTGGACTCCTATGAGCGCATCAAGTCCCAAGAGTGGCCGAGTGTGGGGG 840
QY 916 GACCTTGGGGGAGGAGACCTTTCAGCAGATGGACGAGTTCCTGAAGCTGACCTG 975
Db 841 GACCTTGGGGGAGGAGACCTTTCAGCAGATGGACGAGTTCCTGAAGCTGACCTG 900
QY 976 CTGTGCCCCAGGCCCCAGCATGGCCGGGCTCCGGGGTTCGAGGCTATGCGAGAGCTT 1035
Db 901 CTGTGCCCCAGGCCCCAGCATGGCCGGGCTCCGGGGTTCGAGGCTATGCGAGAGCTT 960
QY 1036 CGGCTTCAGCTTGGAGCGGAAACCCCATCTTTTATGGATCTTTTCCCTCCAGTGGGAA 1095
Db 961 CGGCTTCAGCTTGGAGCGGAAACCCCATCTTTTATGGATCTTTTCCCTCCAGTGGGAA 1020
QY 1096 GGAGCTGCCATCTCTGCTGTGTGCTTCCGACACCCCAAGACATCGGGCAGTGTGAAT 1155
Db 1021 GGAGCTGCCATCTCTGCTGTGTGCTTCCGACACCCCAAGACATCGGGCAGTGTGAAT 1080
QY 1156 GGTCCCTTTAGAGAGCTAAACATGACTGCAACAGGGGACTGCCCTGTCATGGACACAG 1215
Db 1081 GGTCCCTTTAGAGAGCTAAACATGACTGCAACAGGGGACTGCCCTGTCATGGACACAG 1140
QY 1216 GTGCCCCAGCCAGACCTGGAGAGTGCATCGCCCAACACATGAAGCTCAGCAGTTTGA 1275
Db 1141 GTGCCCCAGCCAGACCTGGAGAGTGCATCGCCCAACACATGAAGCTCAGCAGTTTGA 1200
QY 1276 TCCTCACTCTCCCTGCCAGACCGCTGTCTACCTTTATCAGAGACACCTCTCATGGAC 1335

Db 1201 TCCTCACTCTCCCTGCCAGACCGCTGCTCACCTTTATCAGAGACCACTCTCATGGAC 1260
QY 1336 AGCCCGCTGTTCCTCGCTGACGCCGCCCTCTGCTACTACAGATACAGCTATCTC 1395
Db 1261 AGCCCGCTGTTCCTCGCTGACGCCGCCCTCTGCTACTACAGATACAGCTATCTC 1320
QY 1396 AGAGTCTGTGGCCACAGGGGTGACAGCTCTTCAGGGAAGAATATGACGTGCTTACCTG 1455
Db 1321 AGAGTCTGTGGCCACAGGGGTGACAGCTCTTCAGGGAAGAATATGACGTGCTTACCTG 1380
QY 1456 GGCACAGAGGATGACACCTCCACCGGCTGTCGGATTTGGAGCTCAGCTCAGTGTCTTG 1515
Db 1381 GGCACAGAGGATGACACCTCCACCGGCTGTCGGATTTGGAGCTCAGCTCAGTGTCTTG 1440
QY 1516 GAGGATCTGGCTTGTTCAGAAACACAGCCGGTTGAGAGCATGAATTTGTACACAGAT 1575
Db 1441 GAGGATCTGGCTTGTTCAGAAACACAGCCGGTTGAGAGCATGAATTTGTACACAGAT 1500
QY 1576 TGGCTCCTGTGGCTCCCATCTGAGGTGACAAAGTGAACACCAAGCACTGTGGCCGT 1635
Db 1501 TGGCTCCTGTGGCTCCCATCTGAGGTGACAAAGTGAACACCAAGCACTGTGGCCGT 1560
QY 1636 CTCCAGAGCTGCTCGAGTGTATCTCTGGCCAGGACCCGCTGTCGCTGGAGCTTCCGG 1695
Db 1561 CTCCAGAGCTGCTCGAGTGTATCTCTGGCCAGGACCCGCTGTCGCTGGAGCTTCCGG 1620
QY 1696 CTGTAGTCTGTGTGGCCACGCGGAGCAGCCGGGATGTTCAAGATATAGAGTCA 1755
Db 1621 CTGTAGTCTGTGTGGCCACGCGGAGCAGCCGGGATGTTCAAGATATAGAGTCA 1680
QY 1756 GGGGATGTCTCTTCTTTGTGTCAAAAGAACCTGGAGAACATCCCTAGTGTTTGAAGTT 1815
Db 1681 GGGGATGTCTCTTCTTTGTGTCAAAAGAACCTGGAGAACATCCCTAGTGTTTGAAGTT 1740
QY 1816 CGGCTGCTACTGTGGCCAGCTGTGCTTCCCATGTTCCCCAGTTCCTGCCGGGATCC 1875
Db 1741 CGGCTGCTACTGTGGCCAGCTGTGCTTCCCATGTTCCCCAGTTCCTGCCGGGATCC 1800
QY 1876 TGTGTGTGCACAGCCAGTGGAGTGTGCTCCTCCTCCCGAGGATGAGCTAGAG 1935
Db 1801 TGTGTGTGCACAGCCAGTGGAGTGTGCTCCTCCTCCTCCCGAGGATGAGCTAGAG 1860
QY 1936 GTGGTGTGACCCAGGGCCATGGGGCTTATGCTTGGAGTGTTCAGAGGGTGGAGCC 1995
Db 1861 GTGGTGTGACCCAGGGCCATGGGGCTTATGCTTGGAGTGTTCAGAGGGTGGAGCC 1920
QY 1996 GCGCGGTGCTGCTGCTTATAGCTTGGTGTGGGCGAGCAGCGGAGCCCTCAAAACCG 2055
Db 1921 GCGCGGTGCTGCTGCTTATAGCTTGGTGTGGGCGAGCAGCGGAGCCCTCAAAACCG 1980
QY 2056 GCCACACAGTGTGGGGCTGGATTTGGCTTTCTCCTGGGTGTTCTTGACAGATCC 2115
Db 1981 GCCACACAGTGTGGGGCTGGATTTGGCTTTCTCCTGGGTGTTCTTGACAGATCC 2040
QY 2116 CTCACCTCCTCCTGATTTGGTTCGCTCAGCAGCTGCGGACAGAGGAGCTTTAGCT 2175
Db 2041 CTCACCTCCTCCTGATTTGGTTCGCTCAGCAGCTGCGGACAGAGGAGCTTTAGCT 2100
QY 2176 ACAGACAGGTTGGGCTTAGATCTGGGGCTCCACCTTCTGGGACCAAGCTATAGTCAG 2235
Db 2101 ACAGACAGGTTGGGCTTAGATCTGGGGCTCCACCTTCTGGGACCAAGCTATAGTCAG 2160
QY 2236 GACCTCCTCCTCCTTCGCTTGAAGATGAACGGCTGCCCTGCCCTGGGTAAAGCGGGC 2295
Db 2161 GACCTCCTCCTCCTTCGCTTGAAGATGAACGGCTGCCCTGCCCTGGGTAAAGCGGGC 2220
QY 2296 AGTGGTTTGGTGGCTTCCCTCCACCTTCCTGCTGGATTTTGGCCAAAGCCAGCCAC 2355
Db 2221 AGTGGTTTGGTGGCTTCCCTCCACCTTCCTGCTGGATTTTGGCCAAAGCCAGCCAC 2280
QY 2356 ATCCGGCTCAGTGGGGCGCTCTAGCCAGTGTGATGAGACCTCCATCTAA 2406
Db 2281 ATCCGGCTCAGTGGGGCGCTCTAGCCAGTGTGATGAGACCTCCATCTAA 2331

Qy	853	TCCGAGTGTGGACTCCTATGAGCGCATCAAGGTCCCAAGATGGCCCGAGTGTGTGGC	912
Db	781	TCCCGAGTCTTGGACTCATATGAGCGCATCAAGGTCCCAAGATGGCCCGAGTGTGTGGC	840
Qy	913	GGGACCTTGGGGCAGGAAGACCTTCACAGAGATGGACGAGTTCTTGAAGGCTGAC	972
Db	841	GGGACCTTGGGGCCGGAAGACCTTCACAGAGATGGACGAGTTCTTGAAGGCTGAC	900
Qy	973	CTGCTGTGCCAGGGGCCGAGCATGGCCGGGCCCTTCGGGGTTCTGCAAGGCTATGGCAGAG	1032
Db	901	CTGCTGTGTCCAGGGCCCGAGCATGGAAGGGCCCTCGGGGTTCCTGCAGGATATGACAGAG	960
Qy	1033	CTTTCGGCCTCAGCCTCGAGCGGAACCCCCATCTTTTATGGGATCTTTTCTCCCACTGG	1092
Db	961	CTTTCGAGCTCAGCCTGGCGGGGAGCCCCCTCTTTTATGGCATCTTTTCTCCCACTGG	1020
Qy	1093	GAAGGAGCTGCCATCTCTGCTGTGTGTGCCCTTCGGACCCCAAGACATCCGGCAGTCTGTG	1152
Db	1021	GAAGGACCGGCATTTCTGCTGTGTGTGCCCTTCGGACCCCAAGACATCCGGCAGTCTGTG	1080
Qy	1153	AATGGTCCCTTTAGAGAGCTAAACATGACTGTGCAACAGGGAGTGCCTGTCTATGGACAAC	1212
Db	1081	AATGGTCCCTTTAGAGAGCTAAACATGACTGTGCAACAGGGAGTACCCTGTCTATGGACAAC	1140
Qy	1213	GAGTGTCCCGACGCCAGACCTTGAGAGTGTGATGCCCAACAACTGAAGCTCCACGACGTTT	1272
Db	1141	GAGTGTCCCGACGCCAGACCTTGGAGTGTGATCACCACAACTGAAGTTCCACGACGTTT	1200
Qy	1273	GGATCTCACTCTCCCTGCCAGACCGCGTCTCACCTTTATCAGAGACCACTCTCTCATG	1332
Db	1201	GGATCTCTCACTCTCCCTGCCAGACCGTGTCTCACCTTTATCAGAGACCACTCTCATG	1260
Qy	1333	GACAGCCCGTGTCCCGCTGACGGCCGCCCTCTGCTGCTCACTACAGATACAGCCTAT	1392
Db	1261	GACAGCCCGTGTTCAGCTGTATGGCGGCCCTCTGCTGCTCACTACGGATACAGCCTAT	1320
Qy	1393	CTCAGAGTCTGTGCCCAACAGGGTGACAGCCTCTCAGGGAAAGAAATATGACGTCTCTAC	1452
Db	1321	CTCAGAGTTGTGCTCTACCGGGTGACCAGCCTCTCAGGGAAAGAAATATGATGTCTCTAC	1380
Qy	1453	CTGGGACACAGAGATGGACACTTCCACCGGGCTGTGGGCATTTGGAGCTCAGCTCAGTCTC	1512
Db	1381	CTGGGACACAGAGATGGCACCTTCCATCGGGCTGTGGGCATTCGGAGCTCAGCTCAGTCTC	1440
Qy	1513	TTGGAGATCTGGCCTTGTTCACAGAACACAGCCGTTGAGAGCATGAATTTGTATCCAC	1572
Db	1441	CTGGAGATCTGGCCTTGTTCGGAAACACAGCCGTTGAAAGCATGAATTTGTATCCAT	1500
Qy	1573	GATTGGCTCTGTGGGCTCCCATATGAGGTTGACACAAGTGAAACACCACTGTGGC	1632
Db	1501	GATTGGCTCTGTGGGCTCCCATATGAGGTTGACACAAGTGAAACACCACTGTGGC	1560
Qy	1633	CGTCTCCAGAGCTGTCTGGAGTGTATCTCGGCCACAGACCCGTTGTCGCTTGAGCCTC	1692
Db	1561	CGTCTCCAGAGCTGTCTCAGAAATGTATCTCGGCCACAGATCCCGTGTGTGCTTGAGCCTC	1620
Qy	1693	CGGCTTGATCTTGTGTGGCCACCGCCGGCAGCACCGCGGGATGTGTTCAAGATATAGAG	1752
Db	1621	CGGCTCGATCTTGTGTGGCCATGCAAGCGGAGCACCGCTGGATGTTTCAAGACATAGAG	1680
Qy	1753	TCAGCGGATCTCTCTTTTGTGTCCAAAAGAACCTGGAGAACATCCGTTAGTGTTTTGA	1812
Db	1681	TCAGCAGATCTCTCTTTTGTGTCCAAAAGAACCTGGAGAACATCCGTTAGTGTTTTGA	1740
Qy	1813	GTTCGGGTGGCTACTGTGGGCCACGTGGTCTCTGCCATTTTCCGCCAGTTCTGTCCCGC	1872
Db	1741	GTTCAGTGGCTACGGTGGGCCAGTGGTCTCTGCCGTGCTCCCCAGTTCTTGCTTGCGCA	1800
Qy	1873	TCCTGTGTGTGGACACAGCCAGTGTGAGTGACTGCGCTCACTCCCCGGAGGATGTGACTA	1932
Db	1801	TCCTGTGTGTGGACACAGCCAGTGTGAGTGACTTTCGCTACCCACCAAGGAGTGGGCTA	1860

Db 1381 CTGGGACAGAGGATGGGACCTCTCATCGGCTGTGGCATCGAGCTCAGCTCAGTGT 1440
Qy 1513 TTGGAGGATCTGGGCTTTTCCAGAACACAGCCGCTTGGAGCATGAATTTGACAC 1572
Db 1441 CTGGAGGATCTGGGCTTTTCCCGAAGAACAGCCGTTTGAAGCATGAATTTGACAT 1500
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Db 1501 GATTGGCTCTGGTGGCTCCCATCTACTAGGTGACACAAAGTGAACACAGCAACTGTGGC 1560
Qy 1633 CGTCTCAGAGCTCTCGAGTGTATCTCGCCAGAACCCGCTGTGCGCTGGAGCTTC 1692
Db 1561 CGTCTCAGAGCTCTCAGATGTATCTCGCCAGGATCCGCTGTGCTGGAGCTTC 1620
Qy 1693 CGGCTTATCTGTGTGGCCACGCGCGAGCACCGCGGATGTTCAAGATATAGAG 1752
Db 1621 CGGCTGATCTGTGTGGCCACGCGCGAGCACCGCGGATGTTCAAGATATAGAG 1680
Qy 1753 TCAGCGGATCTCTCTTTGTGTCCAAAGAACCTGGAGAACATCCCGTAGTGTGAA 1812
Db 1681 TCAGCAGATCTCTCTTTGTGTCCAAAGAACCTGGAGAACATCCCGTAGTGTGAA 1740
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Db 1741 GTTCCAGTGTCTACGTTGGGCGCAGTGTGCTTGGCGTCTCCCGCAGTTCTGCTGGGCA 1800
Qy 1873 TCCTGTGTGGACACAGCCAGTGGAGTGACTGCTGCTACTCCCGGAGGATGGA 1932
Db 1801 TCCTGTGTGGACACAGCCAGTGGAGTGACTGCTGCTACTCCCGGAGGATGGA 1860
Qy 1933 GAGTGTGTGAGCCCGGCGCATGGGGCTTATGCTTGGAGTGTGAGGAGTGA 1992
Db 1861 GAGTGTGTGAGCCCGGCGCATGGGGCTTATGCTTGGAGTGTGAGGAGTGA 1920
Qy 1993 GCGCCCGCTGTGGCTGTATAGCTTGGTGGGCGAGCCAGCGGGACCCCTCAAC 2052
Db 1921 GCGCCCGCTGTGGCTGTATAGCTTGGTGGGCGAGCCAGCGGGACCCCGCAAC 1980
Qy 2053 CGGCGCCACACCGTTGTGGGCTTGGATTTGGTGGCTTCTCTGGGTGTTTGGCAGCA 2112
Db 1981 CGGCGCCACACCGTTGTGGGCTTGGCTGGTGGCTTCTCTGGGTGTTTGGCAGCA 2040
Qy 2113 TCCTCTACTCTCTCTCTGATGTCGCGCTCAGCAGCGTGGGACAGAGGAGTCTTA 2172
Db 2041 TCCTCTACTCTCTCTCTGATGTCGCGCTCAGCAGCGGCGGCGACAGAGGAGTCTTA 2100
Qy 2173 GCTAGACACAGTGGGCTTAGATCTGGGGCTTCCACCTTCTGGGACCCACAAGCTATAGT 2232
Db 2101 GCTAGACACAGTGGGCTTAGATCTGGGGCTTCCACCTTCTGGGACCCACAAGCTATAGC 2160
Qy 2233 CAGGACCTCTCTCTCTCGCTTGAAGATGAACGGCTGCGCTGGCGCTGGTGAAGCGG 2292
Db 2161 CAGGACCTCTCTCTCTCTCCTTCACTGAAGATGAACGGCTGCGCTGGCGCTGGTGAAGCGG 2220
Qy 2293 GGCAGTGGTGTGTGGCTTCCCTTCCACCTTCTCTGCTGATGTTTCCCAAGCCAGCC 2352
Db 2221 GGCAGTGGTGTGTGGCTTCCCTTCCACCTTCTCTGCTGATGTTTCCCGGAGCCAGCC 2280
Qy 2353 CACATCGGCTACTGGGGCGCTCTAGCCAGCTGTGATGAGACCTCCATCTAA 2406
Db 2281 CACATCGGCTACTGGGGCGCTCTAGCCAGCTGTGATGAGACCTCTATCTAA 2334

RESULT 7
US-10-170-235-32596
; Sequence 32596, Application US/10170235
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
; TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
; FILE REFERENCE: CL001380
; CURRENT APPLICATION NUMBER: US/10/170,235

; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 32596
; LENGTH: 3641
; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-32596

Query Match 47.9% Score 1919.6; DB 47; Length 3641;
Best Local Similarity 77.08; Pred. No. 3.5e-251;
Matches 2699; Conservative 0; Mismatches 594; Indels 213; Gaps 21;

Qy 1 GCCAGGCCCGCCAGTAGCGGTAAAGTAGAGGTGCTGGAGCGCCCGCCAGCCCGCCGAC 60
Db 12 GCCAGGCCAGTAGCGGTAGCCCGGGCCCTGAGCAGAGGCGGTAGCTTGGCGCCGACCCGCG 71
Qy 61 CAGCGGAGCCAGAGATGCTTGCAGGGCGGAGGGGCGCCCGCGGGCGCCCGCCGCGCT 120
Db 72 CAGCGGAGCCAAAGATGCGCGGCTCTGCTGCGCGCGCCCGCGGGTCCCGGGCAGCCT 131
Qy 121 CCGGTCTTCCCTTCCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 132 ACAGCCTCGCCCTTCCC-----GCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 176
Qy 181 CCGGTGTGCGCGCGCGCTCCCGCGCTCAGTCCCGAGAACCTCGCTGCGCCATCTCCGAGGCT 240
Db 177 CCGGTATCCCGCGCGCTCCCGCGCTCGGTGCGCCAGAACCTCGCTTCCAACTCTCTGAGGCT 236
Qy 241 GACTCCTATCTACCCCGGTTTGAGCGTCTCATAGTACAACTTACTTCTGCTGCTGCTGCTGCT 300
Db 237 GACTCCTGCTCACCCTGTTGCGAGTCCCTCACACATACAACTTACTTCTGCTGCTGCTGCTGCT 296
Qy 301 GATCCTCCTCCACACACTTTTACGTCGGTGCGGGATAGCATCTTTCGTTTAAACCCCTC 360
Db 297 GATCCTCCTCCACACACTTTTATGTTGGCGCGCGGACACCATCTTTCGTTTATCCCTG 356
Qy 361 CCCTTCTCTGGGAAAGACCCCGAAGATCAGCTGATGTTGCTGAGCTGAGCTGAGCTGAGCTGAG 420
Db 357 CCCTTCTCAGGGAGAGACCCCGCAGGATTTGACTGGATGTTCTCTGAGGCTCACAGACAG 416
Qy 421 AACTGCGAGGAAGCAAGAGAGAGCAATGTACAACTTTTATCCAGATTTCTCGCC 480
Db 417 AACTGTAGGAAGCAAGAGAGAGCAATGTACAACTTTTATCCAGATTTCTCGCC 476
Qy 481 ATTGTCAATGCTCTACCTCTCAGCTGCGGACCTTTCGTTTGTATCCGAAAGTGGGG 540
Db 477 ATTGCCAATGCTCTACCTCTCAGCTGCGGACCTTTCGTTTGTATCCGAAAGTGGGG 536
Qy 541 GTTATTGATGTGCTTCCAGAGTGTGAAGACTTTGAGAGCGCCCGGGGAAATGT 600
Db 537 GTTATTGATGTGCTTCCAGAGTGTGAAGACTTTGAGAGTGGCGGGGAAATGT 596
Qy 601 CTTTTGAGCCAGCTCAACGTCAGCAGCTGTATGCTGGGGCGCTCTCTACACCGCC 660
Db 597 CTTTTGAGCCAGCTCAGCGTCTCAGCAGCTGTATGCTGGGGGCTCTCTATGCTGCC 656
Qy 661 ACTGTGAAGAACTTCTTGGGACTGAGCCCATCATCTCCCGAGCTGTGGGTGCGAGCTGAG 720
Db 657 ACTGTGAAGAACTTCTTGGGACTGAGCCCATCATCTATCACAGAGCAGTGGGTGCGCGAG 716
Qy 721 GACTGGATTGGAACAGAGACCTTGTCTATCTCTGCTTAACTGCTCCAGCCTTTGTGCGAGCT 780
Db 717 GACTGGATTGCGACAGATACCTTGCCTTCTGCTGCTGAACCGCCAGCCTTTGTGCGAGCC 776
Qy 781 ATGGTCTGAGCCAGCTGAGTGGGGGATGAAGATGGAGACATGAATCTTTTTC 840
Db 777 GTGGCCTTTGAGCCAGCCGAATGGGGGATGAAGATGGAGACATGAATCTTCTTCTTC 836
Qy 841 TTACGAGACCTCCCGAGTGTGGACTCTCTATGAGCGCATCAAGTCCCAAGAGTGGCC 900
Db 837 TTACGAGACCTTTCCCGAGCATTTGACTCATAGAGCGCATTAAGTCCCGAGGCTGGCC 896
Qy 901 CGAGTGTGTGCGGGGACCTTTGGGGCGAGGAAGACCTTTCAGCAGAGATGGACGACCTTT 960

Db	1153	CGGACAGTGTGAATGTGCTCTTAGAGAACTAAACATGACTGCAACAGAGACTGCCT	1212
Qy	1201	GTCATGTGACAAACAGAGTGCCTCCAGCCAGACCTGGAGAGTGCATCGCCAAACAACATGAAG	1260
Db	1213	GTCGTGACAAATGATGTGCCCCAGCCAGACCTGGAGAGTGCATCAACAAACAATGAAG	1272
Qy	1261	CTCCAGCAGTTTGGATCTCACTCTCCCTGCCAGACCGCGTGTCTACCTTTATCAGAGAC	1320
Db	1273	CTCCGGCACITTTGGCTCATCTCTCCCTGCTGACCGCGTACTCACCTTCATCCGGGAC	1332
Qy	1321	CACCTCTCATGACAGCGCCGTGTTCCCGGCTGACGGCGCCCTGCTGTGTCACATA	1380
Db	1333	CACCACCTCATGGACAGCGCAGTGTTCACAGCTGATGGCCACCCTGCTGTGTCACATA	1392
Qy	1381	GATACAGCCTATCTCAGAGTGTGGCCACAGAGGTGACACGCTCTCAGGAAAGAATAT	1440
Db	1393	GATACAGCCTATCTCAGAGTGTGGCCACAGAGGTGACAGCCTCTCAGGAAAGAATAT	1452
Qy	1441	GACGTGCTTACCTGGGACAGAGATGGACACTCCACCGGCTGTGGCGATTGGAGCT	1500
Db	1453	GATGTGCTTACCTGGGACAGAGATGGACACTCCACCGGCTGTGGCGATTGGAGCT	1512
Qy	1501	CAGCTAGTGTCTTGAGGATCTGGCGTTGTTCCCAAGAACACAGCGGTTGAGAGCAT	1560
Db	1513	CAGCTACGCTTCTTGAAGATCTGGCGTTATTCACAGAGCCACAGCGAGTTGAGAACATG	1572
Qy	1561	AAATTGTACCAGATTTGGCTCTGTGGGCTCCATACTCAGGTGACACAGTGAACACC	1620
Db	1573	AAATTGTACCAGACTGGCTCTGTGGTCCCGTACTGAGGTGACACAGTGAATACA	1632
Qy	1621	AGCAACTGTGGCGTCTCCAGAGCTGCTCGGAGTGTATCTGTGCCAGGACCCGCTGTGC	1680
Db	1633	ACCAACTGTGGCGTCTCCAGAGCTGCTCAGAGTGCATCCTGTGCCAGGACCCAGTCTGT	1692
Qy	1681	GCCTGGAGCTTCGGCTTGATGTGTGTGGCCACGCGCGGACGACCGCGGATGGT	1740
Db	1693	GCCTGGAGCTTCGGCTTGSATGATGTGTGGCCCATGTGGCGGAGCAGCGAGGTGGTC	1752
Qy	1741	CAAGATATAGATCAGCGGATGTCCTCTCTTGTGCCAAAGAACTCGAGAACATCCC	1800
Db	1753	CAAGACATAGATCAGCAGATGTCCTCTTGTGTCTTAAGAGCTTGAGAACGTCCA	1812
Qy	1801	GTAGTGTTTGAAGTTCGGTGGCTACTGTGGGCCAGTGTCTGTGCATGTTCCCCAGT	1860
Db	1813	GTAGTGTTTGAAGTTCCTCGTGGCTACAGCTGCGCATGTGTCTTGCCATGTTCTCAAGC	1872
Qy	1861	TCGTCCCTGGCATCTGTGTGTGGCAGCAGCCAGCCAGTGGAGTGACTCGGCTCACTCCCCGG	1920
Db	1873	TCAGCATGGCATCTGTGTGTGGCAGCAGCCAGTGGAGTGACTCACTCACTCCCCCGG	1932
Qy	1921	AGGATGGACTAGAGTGTGTGTGACCCAGGGGCCATGGGGCTTATGCTTGGAGTCT	1980
Db	1933	CGGATGGACTAGAGTGTGTGTGACCCAGGGGCCATGGGGCTTATGCCCTGTGAATGT	1992
Qy	1981	CAGGAGGTGGAGCCCGCGTGGTGTCTTATAGCTTGGTGTGGGACGACGACGG	2040
Db	1993	CAGGAGGTGGGACGCCCATGTGTTAGCAGCTTACAGCTTGGTATGGGACGACGACA	2052
Qy	2041	GGACCTCAAACCGGGCCACACCGTTGTGGGGGCTGGATGTGGTGGCTTCTCTGGGT	2100
Db	2053	GATGCTCCGAGCCGGGCCACAC- --AGTGGGGCGGGACTGGCTGGCTTCTTGTGGG	2109
Qy	2101	GTCTTGTGACATCCCTCACTCCTCTTGTGTCGCTGATGGTCCGCTCAGCAGGCTGGGACAG	2160
Db	2110	ATTCTGCGACATCCCTGACTCTCATCTTGTGTTGGTGTGGGCTGACGAGGACGCGGACAG	2169
Qy	2161	AGGAGCTTCTAGCTAGACAAAGTGGGCTTAGATCTGGGGCTCCTACCTTCTGGGACC	2220
Db	2170	AGGAACTTCTGCTTAGACAAAGTGGGCTTGACCTGGGGCTCCACCTTCTGGGACC	2229
Qy	2221	ACAAGCTATAGTCAGGACCTCCCTCTCCTTCCCTTGAAGATGAACGGCTGCCCTGGCC	2280

D	b		2230	ACAAGCTACAGCCCAAGACCCTCCCTCCCCCTCCTGAAGATGAGCGGTTCGCCGCTGGGC	2289
Q	y		2281	CTGGTAAAGCGGGCACGTGGTTTGTTGGCTTCCTCCACCCCTTCCTGCTGGGATTCTTGC	2340
D	b		2290	CTGCCAAGAGGGCATGGCTTGGTGATTTCCACCACCCCTTCCTGCTTGATCTTGC	2349
Q	y		2341	CAAAGCCCAGCCCACATCCGGCTCACTGGGGCGCCCTTAGCCACAGTGTGATGAGACTCC	2400
D	b		2350	CAAAGCCCAGCCCACATTCGGCTAACCTGGGGCTCTCTAGCCACATGTGATGAACATCC	2409
Q	y		2401	ATCTAAAGCCGGGAAAAATGACTGCCAGCCATGAGCAGTCTCTTGGAAAC	2448
D	b		2410	ATCTAGAGCTGGGCAATGATCCACTAGTGTAATAAGTGATCACTGGAAC	2457
RESULT 9					
US-10-305-278-65					
; Sequence 65, Application US/10305278					
; GENERAL INFORMATION:					
; APPLICANT: OTA, TOSHIO					
; APPLICANT: ISOGAL TAKAO					
; APPLICANT: NISHIKAWA, YETSUO					
; APPLICANT: KAWAI, YURI					
; APPLICANT: SUGIYAMA, TOMOYASU					
; APPLICANT: HAYASHI, KOJI					
; TITLE OF INVENTION: SECRETORY PROTEIN OR MEMBRANE PROTEIN					
; FILE REFERENCE: 084335/0121					
; CURRENT APPLICATION NUMBER: US/10/305,278					
; CURRENT FILING DATE: 2002-11-27					
; PRIOR APPLICATION NUMBER: US/09/611,523					
; PRIOR FILING DATE: 2000-07-07					
; PRIOR APPLICATION NUMBER: JP 1999-194179					
; PRIOR FILING DATE: 1999-07-08					
; PRIOR APPLICATION NUMBER: JP 2000-118775					
; PRIOR FILING DATE: 2000-01-11					
; PRIOR APPLICATION NUMBER: JP 2000-183766					
; PRIOR FILING DATE: 2000-05-02					
; PRIOR APPLICATION NUMBER: 60/159,586					
; PRIOR FILING DATE: 1999-10-18					
; PRIOR APPLICATION NUMBER: 60/183,323					
; PRIOR FILING DATE: 2000-02-17					
; NUMBER OF SEQ ID NOS: 679					
; SOFTWARE: PatentIn Ver. 2.1					
; SEQ ID NO 65					
; LENGTH: 2971					
; TYPE: DNA					
; ORGANISM: Homo sapiens					
; FEATURE:					
; NAME/KEY: CDS					
; LOCATION: (103)..(2412)					
US-10-305-278-65					
Query Match 46.8%; Score 1875.2; DB 50; Length 2971;					
Best Local Similarity 86.1%; Pred. No. 3.8e-245;					
Matches 2107; Conservative 0; Mismatches 323; Indels 18; Gaps 2;					
Qy	1	GCGAGGCGCGCGCAGTAGCGGTACTAAGTAGAGGCTGTGGACGCGCGCCACCCCGGCAC	60		
D	b	28	GCGAGGCCAGTAGCCCCGGGCGCTTAGCAGAGGCGCGTAGTTGCGCGCCGACCCCGCGC	87	
Qy	61	CAGGCGGAGCCAGAGATGCTTGCAGGGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCT	120		
D	b	88	CAGGCGGAGCCAAGATGCGGCGCTCTGCTGCGCGCGCGCGCGCGCGCGCGCGAGCCT	147	
Qy	121	CCGGTCTTTCCTCCCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	180		
D	b	148	ACAGSCCTCGCGCTTCC-----GCTACTGCTGCTGCGGTGCTGAGCGGC	192	
Qy	181	CCGGTGTGGGCGCGCTCCCGCGCTCAGTGCCGAGAACCTCGCTGCCCATCTCCGAGGCT	240		
D	b	193	CCGGTATCGGCGCGCGCTCCCGCGCTCGGTGCGCCAGAACCTCGCTTCCAATCTCTGAGGCT	252	
Qy	241	GACTCTATCTCACCCGGTTTTTGAGCGGCTCTCATACGTAACAATTACTCTGCTCTTGTG	300		

Query Match 46.88; Score 1875.2; DB 50; Length 2971;

BEST LOCAL SIMILARITY	60.1%;	FREQ. NO.	3.0E-243;
MATCHES 2107;	Conservative	0;	Mismatches 323;
			Indels 18; Gaps 2;

1 GCCGAGGCCCGGCAGTAGCGGTACTAAGTAGAGGCTGCTGGACGCGCCCCACCCGGCAC 60

b 28 GCGAGGCCAGTAGCCCCGGGGCCCTGAGCAGAGGCCGTAGCTTGGCGCGCACCGCGGCG 87

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I48 ACAGCCACGCCCTTCCC-----GCTACCTGCTGCCTGGCGGTGCTGAGCGGC 192

181 CCGGTGTGGCGCGCGGTCCCCCGCTCAGTGCCCAAGAACCTCGCTGCCCATCTCCGAGGCT 240
y

b 193 CCGGTATCCGGCGCGGTCCCCCGCTCGGTGCCAGAACCTTCGCTTCCAATCTCTGAGGCT 252

241 GACTCCTATCTCACCCGGTTTGCAGCGTCTCATACGTACAATTACTCTGCTCTCCTTG 300

[illegible]

Db	1333	CACCCACTCATGAGCAGGCCAGTGTCTTCCAGCTGATGGCCACCCCTGCTGGTCACTACA	1399
Qy	1381	GATACAGCCTATCTCAGAGTCGTGGCCACAGAGGTGACCAAGCTCTCAGGGAAGAATAT	1440
Db	1393	GATACAGCCTATCTCAGAGTCGTGGCCACAGAGGTGACCAAGCTCTCAGGGAAGAAGTAT	1452
Qy	1441	GAGCTGCTCTACCTGGGGACAGAGGATGGACACCTCCACGGGCTGTGGGCATTTGAGAGCT	1500
Db	1453	GATGTGCTACTCCTGGGGACAGAGATGGACACCTCCACGGAGCAGTGCAGATCGGAGCT	1512
Qy	1501	CAGCTCAGTCTCTGGAGGATCTGGCCCTTGTTCACAGAACCCACAGCCGTTTGAGAGCATG	1560
Db	1513	CAGCTCAGCCTCTTGAAGATCTGGCCTTATTCACAGAGCCACAGCCAGTTGAGAATCT	1572
Qy	1561	AAATTGTACCACGATTTGGCTTCCTGGTGGGCTCCCATACTGAGGTGACACAAGTGAACACC	1620
Db	1573	AAATTGTACCACAGCTGCTCTGGTTGGCTCCCGTACTGAGGTGACACAAGTGAATACA	1632
Qy	1621	AGCAACTGTGGCCGCTCTCCAGAGCTGCTCGGAGTGATCTCTGGCCACAGGACCCGCTGTC	1680
Db	1633	ACCAACTGTGGCCGCTCTCCAGAGCTGCTCAGAGTGATCTCTGGCCACAGGACCCAGTCTGT	1692
Qy	1681	GCCTGGAGCTTCGGGCTTGATGCTTGTGTGGCCACCGCCGCGCAGCACACC CGGGATGGTT	1740
Db	1693	GCCTGGAGCTTCGGGCTTGGATGATGTGTGGCCCATGTGTGGCCCATGCCGGGAGCACCGAGGTTGGTC	1752
Qy	1741	CAAGATATAGAGTCAGCGGATGTCTCTCTTTGTGTCCAAAGAACCTGGAGAACATCCC	1800
Db	1753	CAGACATAGAGTCAGCAGATGTCTCTCTTTGTGTCTTAAAGAGCCTGGAGAACCTGCCA	1812
Qy	1801	GTAGTGTTTGAAAGTTCCGGTGGCTACTGTGGGCCACGTGGTCTCTGCCATGTTCCCCAGT	1860
Db	1813	GTAGTGTTTGAAAGTTCCCGTGGCTACAGCTGCGCATGTGTCTTGGCATGTTCTCCAAGC	1872
Qy	1861	TCGTCCCTGGGATCCTGTGTGTGCACCCACCCAGTGGAGTGACTGGGCTCACTCCCCGG	1920
Db	1873	TCAGCATGGGCATCTCTGTGTGGCACACGCCAGCCAGTGAGTGACTGCACTCACCCGCCCGG	1932
Qy	1921	AGGATGGACTAGAGGTGGTGGTGACCCAGGGCCATGGGGCTTATGCTTCGCGAGTGT	1980
Db	1933	CGGATGGACTGGAGTGGTGGTGACCCAGGGGCCATGGGGCGCTTATGGCTGTGAATGT	1992
Qy	1981	CAGAGGGTGGAGCCGCCCGCTGGTGGCTGTATATAGTGTGGTGAGGACGCCACGCCG	2040
Db	1993	CAGAGGGTGGGACGCCCATGTGGTAGCAGCTTACAGCTTGTGTGGGACGCCACGCCA	2052
Qy	2041	GGACCTCAAAACGGGCCCCACACGTTGTGGGGGCTGGATGGTTGGCTTTCCTCGGTT	2100
Db	2053	GATGTCTCCGAGCCGGGCCACAC- --AGTGGGGGGGGAGCTGGCTGGCTTCTTTTGGGG	2109
Qy	2101	GTTCCTTCAGCATCCCTCACTCTCTCTCTCATTTGGTCGCCGTACAGAGCCTCGCGCACAG	2160
Db	2110	ATTCTCGCAGCATCCCTCACTCTCATTTCTGATTTGGTGGGCTCAGCAGCAGCGGCACAG	2169
Qy	2161	AGGAGCTTCTAGCTAGAGACAAGTGGGCTTAGATCTGGGGGCTCCACCTTCTGGGACC	2220
Db	2170	AGGGAATCTCTGGCTAGAGACAAGTGGGCTTGACCTGGGGCTCCACCTTCTGGGACC	2229
Qy	2221	ACAAGCTATAGTCAGGACCTCTCCTCTCTCCCTTCCGCTGAAGATGAAGGCTGCCCTTGGCC	2280
Db	2230	ACAAGCTACAGCCAAAGACCTCCCTCCCTCTCTCTGAAGTAGGGGTTTGGCGCTGGCC	2289
Qy	2281	CTGGGTAAAGCGGGCAGTGGTTTTGGTGGCTTCCCTCCACCCCTCTCTGCTGGATCTTTGC	2340
Db	2290	CTGGCCAAAGAGGGCAGTGGCTTTGGTGGATTTCTACACCCCTTCTCTGCTTGAATCTTGC	2349
Qy	2341	CCAAGCCACGCCACATCCGGCTCACTGGGGCGCCCTTAGCCACGTGTGATGAGACCTCC	2400
Db	2350	CCAAGCCACGCCACATTCGGCTAACTGGGGCTCCTTAGCCACATGTGATGAACATCC	2409
Qy	2401	ATCTAAAGCGGGAAATGACTGCCAGCCATGAGCAGTCTCTGGAAAC	2448
Db	2410	ATCTAGAGCTGGCAAAATGACACTAGTGTGATGAAGTATGACCTGCACTGGAAAC	2457

	Query Match	41.8%;	Score 1673.6;	DB 16;	Length 2893;
	Best Local Similarity	82.2%;	Pred. No. 8.9e-218;		
	Matches 2012;	Conservative	0;	Mismatches 319;	Indels 117; Gaps 3;
QY	1	GCGGAGGCCCGCAGTAGTACGGGTACTAAGTATAGAGGCTGCTGGAGCGCGCCACACCGCGCAC	60		
DB					
DB	35	GCGGAGGCCAGTAGCCCCGGGGCCCTGAGCAGAGCGGTAGCTTTGCGCGCACCGCGGC	94		
QY	61	CAGCGGAGCCACAGATGCTTGCAGGCGCAGCGGCCCGCGCGCGCCCGCCGCCGCCCT	120		
DB					
DB	95	CAGCGGAGCCAAAGATGCCGGCCTCTGCTGCGCGGCCCGCGCGGTGCGGGCAGCCT	154		
QY	121	CCGGTCTTTTCCCTTCCCGCGCGCGCTGTCGCTGCTGCTGCTGCGGATACTAAGCGCC	180		
DB					
DB	155	ACAGCCTCGCCCTTCCC-----GCTACTGCTGCTGGCGGTGCTGAGCGGC	199		
QY	181	CCGGTGTGGCGCGCGTCCCGCCTCAGTGCCCCAGAACCTCGCTGCCCATCTCCGAGGCT	240		
DB					
DB	200	CCGGTATCCGCGCGCGTCCCGCCTCGGTGCCAGAACCTCGCTTCCAATCTCTGAGGCT	259		
QY	241	GACTCTATCTACCCGGTTTGACGGCTCTCATAGTACAATTAATCTGCTCTGCTTGTG	300		
DB					
DB	260	GACTCTGTCTACCCGGTTGCGAGTGCCCTCACACATACAAATTAATCTGTTCTCTTGTG	319		

Db	1301	 GATACAGCCTATCTCAGAGTCTGGGCCACAGGGTGACCAGCTCTCAGGGAAGAGTAT	1360
Qy	1441	GAGCTGCTCTACCTGGGGACAGAGTAGACACCTCCACCGGCTGTGCGCATTTGAGCT	1500
Db	1361	GATGTCTCTACTCTGGGACAGAGTAGACACCTCCACCGCAGTGGGATCGGAGCT	1420
Qy	1501	CAGCTCAGTGTCTTTGAGGAGTCTGGGCTTTGTTCCCAAGAACCCAGCGGTTGAGAGCATG	1560
Db	1421	CAGCTCAGCGTTCTTTGAAGATCTGGGCTTATTTCCAGAGCACCAGCGAGTTGAGAATCT	1480
Qy	1561	AAATTCTACACAGATTTGGCTCTGGTGGGCTCCATACTGAGTGTACACAAAGTGAACACC	1620
Db	1481	AAATTGTACACAGCTTGGCTCTCTGGTGGCTCCGCTACTGAGTGTACAAAGTGAATACA	1540
Qy	1621	AGCAACTGTGGCGTCTCCAGAGCTGCTCGAGTGTATCTTGCCCGCAGGACCCCGTGTGC	1680
Db	1541	ACCAACTGTGGCGTCTCCAGAGCTGCTCAGAGTGCATCTTGCCCGCAGGACCCAGTCTGT	1600
Qy	1681	GCCTGAGCTTCGGGCTTTGATGTTGTGTGGCCACGCGCGGAGAGACACCGGGATGGTT	1740
Db	1601	GCCTGAGCTTCGGGCTTGATGATGTGTGGCCATGCGCGGAGACCCGAGGTTGGTC	1660
Qy	1741	CAAGATATAGATCAGCGATGTCCTCTTTCTGTGTCCTCAAAAGAACTGGAGAACATCCC	1800
Db	1661	CAAGACATAGATCAGCAGATGTCCTCTTTGTGTCTTAAAGAGCCTGGAGAACGTCCA	1720
Qy	1801	GTAGTGTTTGAAGTTCCGGTGGCTACTGTGGGCGACGTGCTCTGCCATGTTCCCCAGT	1860
Db	1721	GTAGTGTTTGAAGTTCCCGTGGCTACAGCTGCCGATGTGTCTTGCCATGTTCTCCAAGC	1780
Qy	1861	TCGCTCTGGGCATCTCTGTGTGTGGACACAGCCAGTGGAGTGACTGGCTCTACTCCCGG	1920
Db	1781	TCAGCATGGGCATCTCTGTGTGGCACCAAGCCAGTGGAGTGACTGCACTCACCCCGG	1840
Qy	1921	AGGATGGACTAGAGCTGTGTGTGACCCAGGGCCATGGGGCTTATGCTTGGAGTGT	1980
Db	1841	CGGGATGGACTGAGGTGGTGTGGACCCAGGGCCATGGGGCTTATGCTCTGTAATGT	1900
Qy	1981	CAGGAGGTGGACCCCGCGTGGTGTCTTATAGCTTGTGTGGGCGAGCCAGCGG	2040
Db	1901	CAGGAGGTGGGCGAGCCCATGTTGGTAGCAGCTTACAGCTTGTGTATGGGCGACCCAGCA	1960
Qy	2041	GGACCTCAACCGGGCCACACCGTTGTGGGGCTGGATGGTTGGCTTCTCTGGGT	2100
Db	1961	GATGCTCCGAGCGCGGCCACAC- --AGTGGGGCGGAGTGGCTGTCTTCTTGGG	2017
Qy	2101	GTCTTTGCAGCATCCCTCACTCTCCTCTGATTTGTCGCGTCAGCAGCTCGGCGACAG	2160
Db	2018	ATTCTCGCAGCATCCCTGACTCTCATCTTGATTTGGTGGCGTTCAGCAGCCAGCGACAG	2077
Qy	2161	AGGAGCTTCTAGCTAGACAAAGTGGGCTTAGATCTTGGGGCTCCACCTTCTGGGACC	2220
Db	2078	AGGGAATCTTGCTAGAGCAAAGTGGGCTTGACCTGGGGCTCCACCTTCTGGGACC	2137
Qy	2221	ACAAGCTATAGTCAGACCTCCCTCTCTTCCGCTGAAGATGAACGGCTGCCCTGGCC	2280
Db	2138	ACAAGCTACAGCCAAGACCTCCCTCCCTCTCTCTGAAAGTAGAGCGGTTGCGGCTGGCC	2197
Qy	2281	CTGGGTAAAGCGGGCAGTGGTTTGTGTGGCTTCCCTCCACCTTCTCTGCTGGATCTTGC	2340
Db	2198	CTGGCAAGAGGGCAGTGGCTTTGTGTGGATCTTCAACACCTTCTCTGCTGTGATCTTGC	2257
Qy	2341	CCAAGCCACGCCACATCCGGCTCACTGGGGCGCCTTAGCCACGTTGTATGAGACCTCC	2400
Db	2258	CCAAGCCACGCCACATCCGGCTAATCGGGCTCTCTAGCCACATGTGATGAACATCC	2317
Qy	2401	ATCTAAAGCGGGGAAATGACTGCCAGCCATGAGCAGTCTCTGGAAC	2448
Db	2318	ATCTAGAGCTGGCAATGACCACTAGTGTATAAGTATAGTCACTCACTGGAAC	2365

```

US-09-160-762-1
; Sequence 1, Application US/09160762A
; GENERAL INFORMATION:
; APPLICANT: David Michaelovich
; APPLICANT: Trudy Rachel Doe
; APPLICANT: Philip David Hayes
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30036
; CURRENT APPLICATION NUMBER: US/09/160,762A
; CURRENT FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2893
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-160-762-1

Query Match      41.8%; Score 1673.6; DB 16; Length 2893;
Best Local Similarity 82.2%; Pred. No. 8.9e-218;
Matches 2012; Conservative 0; Mismatches 319; Indels 117; Gaps 3;

QY      1  GCCAGAGCCGCGCAGTAGCGGTACTAAGTAGAGGCTGCTGGAGCGGCCCCACCCGCGCAC 60
DB      35  GCCAGGCGCAGTAGCCCCGGGGCCCTGAGCAGAGGCGCGTAGCTTGCAGCGCAGCCCGCGGC 94

QY      61  CAGCGGAGCAGCAGAGATGCTTGCAGAGCGCGAGCGGCCGCCCGCGCGGCCCGCGCGCGCGCT 120
DB      95  CAGCGGAGCAGAGATGCGCGCTCTGCTGCGCGGCCGCCCGCGCGCGGTCCGGGCGAGCCT 154

QY     121  CCGGTCTTTTCCCTTTCCCGCGCGCGCTGTGCGTGTGCTGTGTGCGGATACATAAGCGCC 180
DB     155  ACAGCCTCGCCCTTCCC-----GCTAGTGTGCTGGCGGTGCTGAGCGGC 199

QY     181  CCGGTGTGCGGCCCGCGTCCCGCGTCCAGTGCCCGAGACCTCGCTGCCCATCTCCGAGGCT 240
DB     200  CCGGTATCCGGCGCGCGTCCCGCGTCCGTGCCAGAACCTCGCTTCCAATCTCTGAGGCT 259

QY     241  GACTCTATCTACACCGGTTTGGCAGCGTCTCATACGTACAAATTACTCTGCTCTCCTTTGTG 300
DB     260  GACTCTGTCTCACCGGTTGCGAGTCCCTCACACATACAATTACTCTGTTCTCTTTGTG 319

QY     301  GATCCTGCCTCCACACACTTTAGTCCGGTGCACGGATAGCATCTTTCGGCTTTAACCCCTC 360
DB     320  GATCCTGCCTCCACACACTTATGTGGCGCCGGCAGCACCATCTTCGCTTTTATCCCTG 379

QY     361  CCTTCTCTGGGGAAGACCCCGAAGGATCGACTGGATGTGTTACTCTGAGACTCACAGACAG 420
DB     380  CCTTCTCAGGGGAGAGACCCCGAGGATTGACTGGATGGTTCTGTAGGCTTCACAGACAG 439

QY     421  AACTGCAGGAAGAAAGGCAAGAAAGACGAATGTCACAATTTTATCCAGATTTCTGCC 480
DB     440  AACTGTAGGAAGAAAGCAAGAAAG----- 466

QY     481  ATTGTCAATGCCTCTCACTCTCTCACGTGGCGCACCTTCGGCTTTTGTATCCGAAGTGGCGG 540
DB     467  ----- 466

QY     541  GTTATTGATGTGTCAGCTTTCCACGAGGTTGAAAGACTTGAGAGCGGCCCGGGGAAATGT 600
DB     467  -----GATGTGTCCAGGTTCCAGCAGGTTGAAAGACTTGAGAGTGGCCGGGGGAAATGT 520

QY     601  CTTTTAGCCAGCTCAAGCGTCAGCAGCTCTAATGGCTGGGGCGTCTCTCTACACCGCC 660
DB     521  CCTTTTAGCCAGCTCAGCGGTGACGAGCTGTAAATGGCTGGGGGGTCCCTCTATGCTGCC 580

QY     661  ACTGTGAAGAACTTCCCTGGGACTGAGCCCATCATCTCCCGAGCTGTGGGTTCGAGCTGAG 720
DB     581  ACTGTGAAGAACTACCTGGGACGAGGCCAATTATCACCAGAGCAGTGGGTGTCGCGCAG 640

QY     721  GACTGGATTCGAACAGAGACCTTGTCACTCTGGGCTTAATGCTCCAGGCTTTGTGCTGACGT 780
DB     641  GACTGGATTCGACAGATACCTTGCCTTCCGTGAGTGAACGCCCGCCAGGCTTTGTGCGCAGC 700

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QY 781 ATGGTCTGAGCCACGCTGAGTGGGGGATGAAGATGGAGACATGAATCTTTTTC 840
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 701 GTGGCCTTAGGCCACGACCGAATGGGGGATGAAGATGGAGACGACGAATCTTCTTC 760
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 841 TTCACGAGACCTCCCGAGTGTGGACTCCTATGAGCGCATCAAGCTCCCAAGAGTGGCC 900
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 761 TTACCGAGACTCCCGAGCATTTGACTCATAGCGCATTAAGTCCCAAGGGTGGCC 820
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 901 CGAGTGTGTCGGGGGACCTTGGGGCGAGGAAGACCTTTCAGCAGAGATGGACGAGTTT 960
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 821 CGTGTGTGTCGGGGACCTCGGGGCGGAGACCTCCAGCAGAGATGGAGAGTTT 880
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 961 CTGAAGCTGACCTGTGTGCCAGGGCCGAGCATGGCCGGGCTCCGGGTTTCGAC 1020
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 881 TTGAAGCTGACCTGTGTGTCCAGGGCTGAGCATGGCCGGGCTCCAGTGTCTGCAG 940
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1021 GCTATGGCAGAGCTTCGGGCTCAGCTGGAGCGGGAACCCCATCTTTTATGGATCTTT 1080
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 941 GATGTGCTGTCTTCGACCTGAGCTTGGGGGAGGACTCCCATCTTTTATGGCATCTTT 1000
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1081 TCCTCCAGTGGGAAGAGCTGCCATCTCTGTGTGTGCTTCCGACCCCAAGACATC 1140
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1001 TCTTCCAGTGGAGGGGCTACTATCTCTGTGTGTGCTTCCGACCCCAAGACAT 1060
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1141 CGGGCAGTGTGAATGGTCCCTTTAGAGAGCTAAACATGACTGCAACAGGGGACTGCCT 1200
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1061 CGGACAGTGTGAATGGTCCCTTCAGAGAACTAAACATGACTGCAACAGAGAGTGCCT 1120
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1201 GTCATGCAACAGAGTGGCCAGCCAGACCTGGAGAGTGCATGCCAACACATGAAG 1260
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1121 GTCGGGACATGATGTGCCAGCCAGACCTGGAGAGTGCATCACCACACATGAAG 1180
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1261 CTCAGCAGTGTGGATCTCTACTCTCCCTGCCAGACCGGCTGCTCACTTTATCAGAGAC 1320
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1181 CTCGGSCATTTGGTCTATCTCTCTCCCTGCTGACCGGCTACTCACTTTCATCCGGAC 1240
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1321 CACCTCTCATGGACAGGCCGTGTTCGGGCTGAGCGGCCGCCCTGTGTGCTACTACA 1380
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1241 CACCCACTCATGGACAGGCCAGTGTTCAGGTGATGGCCGCCCTGTGTGCTACTACA 1300
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1381 GATACAGCTATCTCAGAGTCTGTGGCCACAGGGTGAACAGCTCTCTCAGGGAAGAAAT 1440
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1301 GATACAGCTATCTCAGAGTCTGTGGCCACAGGGTGAACAGCTCTCTCAGGGAAGAGAT 1360
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1441 GACGTGCTTACTCTGGGACAGAGGATGACACCTCCACCGGCTGTGGCATTTGGAGCT 1500
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1361 GATGTGCTTACTCTGGGACAGAGGATGGACACCTCCACCGAGAGTGGGATCGAGCT 1420
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1501 CAGCTCAGTGTCTGGAGGATCTGGCTTGTTCAGAACACACAGCCGGTTGAGAGCATG 1560
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1421 CAGCTCAGCGTCTTGAAGATCGCCCTTATTTCCAGAGCCACAGCCAGTTGAGAACATG 1480
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1561 AAATTGTACACGATTGGCTCTGTGGCTCCCATCTGAGGTGACACCAAGTGAACACC 1620
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1481 AAATTGTACACAGCTGGCTCTGTGGCTCCCATCTGAGGTGACACCAAGTGAATACA 1540
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1621 AGCACTGTGGCGCTCTCAGAGCTGCTCGGAGTGTATCTCGCCAGGACCCCGTGTGC 1680
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1541 ACCAATGTGGCGCTCTCAGAGCTGCTCAGAGTGCATCTGTGCCAGGACCCAGTCTGT 1600
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1681 GCCTGGAGTTCGGCTTGAATGCTGTGGCCACAGCGGGGAGACCGGGGATGGTT 1740
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1601 GCCTGGAGTTCGGCTTGAATGCTGTGGCCCATGTGCCAGGACCCAGGGTGGTC 1660
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1741 CAAGATATAGAGTACAGCGATGCTCTCTTTGTCTCCAAAGAACCTGGAGAACATCCC 1800
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1661 CAAGACATAGAGTACAGAGATGCTCTCTTTGTCTCTTAAGAGCCCTGGAGAGCTCCA 1720
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1801 GTAGTGTGTAAGTTCCGGTGGCTACTGTGGGCCACGTGGTCTGCCATGTTCCCGCAGT 1860
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1721 GTAGTGTGTAAGTTCCCGTGGCTACAGCTGGCATGTGGTCTTCCCATGTTCTCCAAGC 1780
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
QY 1861 TCTGCCTGGGCATCTGTGTGGCCACAGCCAGTGGAGTGAAGTCTACTCGGTCTACTCCCGG 1920
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1781 TCAGCATGGGCATCTCTGTGTGGCCACAGCCAGTGGAGTGAAGTCTACTCGGTCTACTCCCGG 1840
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1921 AGGGATGGAGTGAAGTGTGTGACCCAGGGGCCATGGGGCTTATGCTTGCAGTGT 1980
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1841 CGGGATGGAGTGAAGTGTGTGACCCAGGGGCCATGGGGCTTATGCTTGTGAATGT 1900
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1981 CAGGAGGTGGAGCCCGCGCTGTGTGCTTATAGCTTGTGTGGGCGAGCCAGCGG 2040
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1901 CAGGAGGTGGGCGAGCCCATGTGTAGCAGCTTACAGCTTGTATGGGCGAGCCAGCA 1960
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2041 GGACCTCTAAACCGGGGCCACACCGTGTGGGGGCTGGATGTGTGGCTTTCCTCGGT 2100
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1961 GATGCTCCAGCCGGGCCACAC - - - AGTGGGGCGGAGCTGGCTGCTTCTTGTGGG 2017
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2101 GTTCTGTGAGCATCTCTCACTCTCTCTCTGATTGGTGGCGCTCAGCAGCGTGGGCCACAG 2160
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2018 ATTCTGCGAGCATCCCTGACTCTCACTCTGATTGGTGGCGCTCAGCAGCGGCGCACAG 2077
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2161 AGGAGCTTCTAGCTAGAGACAAGTGGGCTTAGATCTGGGGCTCCACTTCTTGGGACC 2220
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2078 AGGAACTTCTGGCTAGAGACAAGTGGGCTGGACTGGGCTCCACTTCTTGGGACC 2137
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2221 ACAAGCTATAGTCAGGACCTCTCTCTCTCTCGCTGAAGATGAACGGCTGCCCTGGCC 2280
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2138 ACAAGCTACAGCAAGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2197
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2281 CTGGGTAAAGCGGGGAGTGTGTGGTGGCTTCCCTCCACCTTCTCTCTCTCTCTCTCTCT 2340
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2198 CTGGCCAAAGGGGAGTGGCTTGTGTGATTCTTCAACACCTTCTCTCTCTCTCTCTCTCT 2257
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2341 CCAAGCCAGCCACATCCGGCTCACTGGGGGCGCTCTTAGCCACGCTGTGATGAGACCTCC 2400
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2258 CCAAGCCAGCCACATCCGGCTCACTGGGGCTCTCTTAGCCACATGTGATGAACATCC 2317
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2401 ATCTAAAGCCGGGAAATGACTGCCAGCCATGAGCAGTCTCTGGAAC 2448
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2318 ATCTAGTGGGCAATGACCACCTAGTGTATAAGTGTACTTGGAAAC 2365
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 12

US-09-808-665A-1

```
; Sequence 1, Application US/09808665A
; GENERAL INFORMATION:
; APPLICANT: David Michalovich
; APPLICANT: Trudy Rachel Doe
; APPLICANT: Philip David Hayes
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30036-C1
; CURRENT APPLICATION NUMBER: US/09/808,665A
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/160,762
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 98300693.3
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 9816423.9
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 9816676.2
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2893
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-808-665A-1
```

Query Match 41.8%; Score 1673.6; DB 34; Length 2893;

Best Local Similarity 82.2%; Pred. No. 8.9e-218;

Matches 2012; Conservative 0; Mismatches 319; Indels 117; Gaps 3;

QY 1 GCCGAGGCCCGCGCAGTAGCGGTACTAAGTAGAGGCTCTGTGACGCGGCCACCCCGGCAC 60

QY	1621	AGCAACTGTGGCCGTCCTCAGAGCTGCTGGAGTGTATCTTGGCCGAGACACCCGCTGTGC	1680
Db	1541	ACCAACTGTGGCCGTCCTCAGAGCTGCTCAGAGTGTATCTTGGCCGAGACACCCGCTGTGC	1600
QY	1681	GCCTGGAGCTTCCGGCTTGATCTTGTTGTGGCCACCGCGGCGAGCACCGCGGATGGTT	1740
Db	1601	GCCTGGAGCTTCCGGCTTGGATGAGTGTGTGGCCCATCGCCGGGAGCACCGAGGTTGGTC	1660
QY	1741	CAAGATATAGAGTCAGCGGATGTCCTCTTTGTGTCCAAAAGAACTGTGAGAAATCCC	1800
Db	1661	CAAGACATAGAGTCAGCAGATGTCCTCTTTGTGTCTTAAAGAGCTGTGAGAACTCCA	1720
QY	1801	GTAGTCTTTGAAGTTCCTGGTGTACTGTGGGGCACGTGTGTCTGTGCATGTTCCCCAGT	1860
Db	1721	GTAGTCTTTGAAGTTCCTGGTGTACAGCTGCCCATGTGTCTTGGCATGTTCTCAAGC	1780
QY	1861	TCGTCTTGGGCATCCTGTGTGTGGCACACAGCCCACTGGAGTGACTGGCTTCACTCCCCGG	1920
Db	1781	TCAGCATGGGCATCCTGTGTGTGGCACACAGCCCACTGGAGTGACTGCATCACCCCCCGG	1840
QY	1921	AGGATGTGACTAGAGTGTGTGTACCCAGGGGCCATGGGGCTTATGCTTCGAGTGT	1980
Db	1841	CGGATGTGACTGAGTGTGTGTACCCAGGGGCCATGGGGCTTATGCTTCGTGAATGT	1900
QY	1981	CAGGAGGTGTGAGCCGCCGCTGTGTGTCTTATAGCTTGTGTGGGACGCCAGCGG	2040
Db	1901	CAGGAGGTGTGGGCAGCCATGTGTGTAGCAGCTTACAGCTTGTATGGGACGCCAGCGA	1960
QY	2041	GGACCTCAAAACGGGGCCACACCGTTGTGGGGCTGGATGGTTGGCTTTCCTCTGGGT	2100
Db	1961	GATGCTCCGAGCCGGGCCACAC---AGTGGGGCGGGAGCTGGCTGGCTTCTTCTGGGG	2017
QY	2101	GTCTTTGCAGCATCCCTCACTCTCCCTCTGATTGTGTGCGCGTCAGCAGCGCTCGGCACAG	2160
Db	2018	ATTCTCGCAGCATCCCTGACTCTCATCTTCTGATTGTGTGCGCGTCAGCAGCGCAGCAG	2077
QY	2161	AGGAGCTTCTAGCTAGAGNCAAGTGTGGCTTAGATCTGGGGGCTCCACTTCTGGGACC	2220
Db	2078	AGGGAATCTTGCTTAGAGCAAGTGTGGGCTTGAGCTGGGGGCTCCACTTCTGGGACC	2137
QY	2221	ACAAGCTATAGTCAGGACCCCTCCCTCTCTCTTCGCCCTGAAGATCAAGCGCTGCCCTGGCC	2280
Db	2138	ACAAGCTACAGCCAAGACCCCTCCCTCCCTCTCTCTGAAGATGAGCGGTGCGCGCTGCC	2197
QY	2281	CTGGGTAAAGGGGGCAGTGGTTTTGTGTGGCTTCCCTCCACCCCTTCTGTCTGATTTCTTC	2340
Db	2198	CTGGCCAAAGAGGGGCAGTGGCTTTGTGTGATTCTCACCAACCCCTTCTGTCTGATTCCTTC	2257
QY	2341	CCAAGGCCAGCCACATCCGGCTCACTTGGGGGCCCTCTAGCCACAGTGTGTATGAGACCTCC	2400
Db	2258	CCAAGGCCAGCCACATTCGGCTTAATCTGGGGCTCTCTAGCCACATGTGTATGAAACATCC	2317
QY	2401	ATCTAAAGCGGGGAAAATGACTGCCAGCCATGAGCAGTCTCTGGAAAC	2448
Db	2318	ATCTAGAGCTGGGCAATGACCACTAGTGTATTAAGTATCACTCTGGAAAC	2365

```

RESULT 14
US-9-160-762-3
; Sequence 3, Application US/09160762
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: DOE, TRUDY
; APPLICANT: HAYES, PHILIP
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: US

```

```

; ZIP: 19482-0980
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 24-SEPT-1998
; APPLICATION NUMBER: US/09/160,762
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: EP 98300693.3
; FILING DATE: 30-JAN-1998
; APPLICATION NUMBER: US 9816423.9
; FILING DATE: 28-JUL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-30036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 601-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2894 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-160-762-3

```

Query Match	41.8%;	Score 1673.6;	DB 16;	Length 2894;
Best Local Similarity	82.2%;	Pred. No. 8.9e-218;		
Matches 2012;	Conservative	0;	Mismatches 319;	Indels 117; Gaps 3;

Qy	1	GCGAGGCGCGCAGTAGCGGTACTAAGTAGAGGCTGCTGGAGCGGCCCCACCCGCGCAC	60
Db	35	GCGAGGCCAGTAGCCCCGGGGCCCTGAGCAGAGCGGTAGCTTGCGCCGACCCCGGGC	94
Qy	61	CAGGCGGAGCCAGAGATGCTTGGCAGGGCCGAGCGGCCCGCCCGGCCCGCCGCGCCCT	120
Db	95	CAGGCGGAGCCAAAGATGCCGGCTCTGCTGCGCGGCCCGCCGGGTCCCGGSCAGCCT	154
Qy	121	CCGGTCTTTCCTTCCGCGCGCGCTGCTCCGTGCTGCTGCTGGCGATACATAAGGCC	180
Db	155	ACAGCCTCGCCCTTCC-----GCTACTGCTGCGGGTGCCTGAGCGGC	199
Qy	181	CCGGTGGCGGCGCGCCCGCTCAGTGCCAGAACCTCGCTGCCCATCTCCGAGGCT	240
Db	200	CCGGTATCCGGCGCGCTCCCGCTCGGTGCCAGAACCTCGCTTCCAATCTCTGAGGCT	259
Qy	241	GACTCCTATCTCACCCGGTTTGCAGCGTCTCATACGTTACAATTACTGCTGCTCCTTGTG	300
Db	260	GACTCCTGTCTCACCCGGTTCGCGAGTCCCTCACACATACAAATTACTCTGTTCTCCTTGTG	319
Qy	301	GATCCTGCCCTCCACACACACTTACGTCCGTTGCAGGGATAGCATCTTCGCTTTAACCCCTC	360
Db	320	GATCCTGCCCTCCACACACTTTATGTGGCGCCGGACACCATCTTCGTTTATCCCTG	379
Qy	361	CCCTTCTCTGGGAAAGACCCGAAGGATCGACTGGATGGTACTGAGACTCACAGACAG	420
Db	380	CCCTTCTCAGGGGAGAGACCCCGCAGGATGACTGGATGGTTCTTGAGGCTCACAGACAG	439
Qy	421	AACTGCGAGGAAGAGGCAAGAAAGAGGACGAATGTCACAATTTTTCAGATTCCTGCC	480
Db	440	AACTGTAGGAAGAAAGCAAGAAAG-----	465
Qy	481	ATTGTCAATGCCTCTCACCTCCTCACGTGGCGACCTTCGCTTTGATCGAAGTGGCGG	540
Db	467	-----	466
Qy	541	GTTATTGATGTCCAGTTTCCAGCAGGTTGAAAGACTTGAGAGCGGCCCGGGGAAATGT	600

Qy		1021	GCTATGCCAGACTTGGCCCTCAGCGTCGAGCGGGAACCCCATCTTTTATGGGATCTTT	108
Db		941	GATGTGCTGTGTGCAGCTTGAGCTTGGGGCAGGGACTCCCATCTTTTTATGGCACTTT	1000
Qy		1081	TCTCCCACTGGGAAGGAGCTGCCATCTCTGCTGTGTGTGCTTCCGACCCCAAGACATC	1140
Db		1001	TCYTCCAGTGGGAGGGGGCTACTATCTCTGCTGTGTGTGCTTCCGACCACAAGACATT	1060
Qy		1141	CGGCGAGTGTGAATGGTTCCTTTTAGAGAGCTAAACATGACTGCAACAGGGGACTGCCT	1200
Db		1061	CGGACAGTGTGAATGGTTCCTTCAGAGAATAAACAATGACTGCAACAGAGGACTGCCT	1120
Qy		1201	GTCA TGACAACAGAGTGGCCCCAGCCAGACCTGGAGAGTGATCGGCCAACACAATGAAG	1260
Db		1121	GTG TGACAATGATGTGCCCAAGCCAGCACCTGGAGAGTGATCACCACAACATGAAG	1180
Qy		1261	CTCCAGCAGTTTGGATCCTCAC TCTCCCTGCCAGACCGGTGCTACCTTTATCAGAGAC	1320
Db		1181	CTCCGCACATTGCTCATCTCTCTCCCTGGCTGACCGGTACHACCTTCATCCGGGAC	1240
Qy		1321	CACCTCTCATGGACAGCGCCGTTTCCCGGCTGACGCGCGCCCTGCTGGTCACTACA	1380
Db		1241	CACCCACTCATGGACAGGCCAGTGTTCAGCTGATGCCACACCCCTGCTGGTCACTACA	1300
Qy		1381	GATACAGCCTATCTCAGAGTCTGGGCCACAGAGGTGACCGACTCTCAGGGAAAATAT	1440
Db		1301	GATACAGCCTATCTCAGAGTCTGGGCCACAGAGGTGACCGACTCTCAGGGAAAAGTAT	1360
Qy		1441	GAGTGCTCTACCTGGGGACAGAGGATGGACACCTCCACGGGCTGTGCGCATTTGGAGCT	1500
Db		1361	GATGTGCTCTACCTGGGGACAGAGATGGACACCTCCACCGAGCAGTGGGATCGGAGCT	1420
Qy		1501	CAGCTCAGTGTCTTGGAGGATCTGGCCCTTGTTC CAGAACACAGCCGGTTGAGAGCAT	1560
Db		1421	CAGCTCAGCGTCTTTGAAGATCTGGCCCTTATTCCAGAGCCACAGCCAGTTGAGAACATG	1480
Qy		1561	AAATTGACACAGATTGGCTCCTGGTGGGCTCCCATACTGAGGTGACACAAGTGAACACC	1620
Db		1481	AAATTGTACCAACAGCTGGCTCCTGGTTGGTCCCGTACTGAGSGTGACACAAGTAANTACA	1540
Qy		1621	AGCAACTGTGGCGCTCTCCAGAGCTGCTCGSAGTGTATCTCTGGCCCAAGGACCCGTGTC	1680
Db		1541	ACCNACTGTGGCCGCTCTCCAGAGCTGCTCAGAGTGATCTCTGGCCCAAGGACCCAGTCTGT	1600
Qy		1681	GCCTGGAGCTTCCGGCTTGATGCTGTGTGGCCCAAGCCGCGAGCACC CGCGGATGGTT	1740
Db		1601	GCCTGGAGCTTCCGGCTGGATGAGTGTGTGGCCCATCCCGGGAGCACCGAGGTTGGTC	1660
Qy		1741	CAAGATATAGAGTCAGCGGATGCTCTCTTTGTGTCCA AAGAACCTGGAGACATCCC	1800
Db		1661	CAAGACATAGAGTCAGCAGATGTCTCCTCTTTGTGTCTTAA GAGCCTGGAGAACCTGCA	1720
Qy		1801	GTAGTGTTGAAGTTCGGTGGCTACTGTGGGCCAGCTGTGCTCCCATGTTCCCCAGT	1860
Db		1721	GTAGTGTTGAAGTTCGGTGGCTACTGTGGGCCAGCTGTGCTCCCATGTTCTCCAAGC	1780
Qy		1861	TCTGCCTGGGCATCCTGTGTGTGCACAGCCAGCTGAGTGACTGCCTCACTCCCGGG	1920
Db		1781	TCAGCATGGGCATCCTGTGTGTGCACAGCCCAAGTGGAGTGA CTGCACCTCACCCCCGG	1840
Qy		1921	AGGATGGACTAGAGTGGTGGTGACCCCCAGGGGCCATGGGGGCTTATGCTTGGCAGTGT	1980
Db		1841	CGGATGGACTGGAGTGGTGGTGACCCCCAGGGGCCATGGGGCCTTATGCCGTGTAATGT	1900
Qy		1981	CAGGAGGTGGAGCCCGCGGTGGTGGCTGCTTTATAGCTTGGTGTGGGGCAGCCAGCGG	2040
Db		1901	CAGGAGGTGGGGCAGCCCATGTGGTAGCAGCTTACAGCTTGGTATGGGGCAGCCAGCGA	1960
Qy		2041	GGACCCCTCAAACCGGGCCACACCGTGTGGGGCTGGATGGTGTGGCTTCTCTGGGT	2100
Db		1961	GATGCTCCGACCGGGGCCACAC - - - AGTGGGGGGGAGACTGGCTGGCTTCTTCTGGGG	2017
Qy		2101	GTTCCTTGACAGCATCCCTCACTCTCCTCTCTGATTTGGTGCCTGTCAAGCAGCTGCGCGACAG	2160

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	218	9.4	2433	4	US-09-300-958A-24	Sequence 24, Appl
2	215.2	9.2	4157	4	US-08-556-432A-1	Sequence 1, Appl
3	94.2	4.0	3524	4	US-09-077-940A-3	Sequence 3, Appl
4	79.2	3.4	3692	4	US-09-077-940A-1	Sequence 1, Appl
5	66.6	2.9	2854	1	US-08-121-713D-57	Sequence 57, Appl
6	66.6	2.9	2854	1	US-08-835-268-57	Sequence 57, Appl
7	66.6	2.9	2854	2	US-09-060-692-57	Sequence 57, Appl
8	66.6	2.9	2854	3	US-08-833-391-57	Sequence 57, Appl
9	66.6	2.9	2854	4	US-09-060-610-57	Sequence 57, Appl
10	66.6	2.9	2854	5	PCT-US94-10151A-57	Sequence 57, Appl
11	60.6	2.6	2601	1	US-08-121-713D-53	Sequence 53, Appl
12	60.6	2.6	2601	1	US-08-835-268-53	Sequence 53, Appl
13	60.6	2.6	2601	2	US-09-060-692-53	Sequence 53, Appl
14	60.6	2.6	2601	3	US-08-833-391-53	Sequence 53, Appl
15	60.6	2.6	2601	4	US-09-060-610-53	Sequence 53, Appl
16	60.6	2.6	2601	5	PCT-US94-10151A-53	Sequence 53, Appl
17	57.6	2.5	2898	4	US-09-308-1798B-2	Sequence 2, Appl
18	56.8	2.4	7218	1	US-08-232-463-14	Sequence 14, Appl
19	51.8	2.2	2504	1	US-08-121-713D-63	Sequence 63, Appl
20	51.8	2.2	2504	1	US-08-835-268-63	Sequence 63, Appl
21	51.8	2.2	2504	2	US-09-060-692-63	Sequence 63, Appl
22	51.8	2.2	2504	3	US-08-833-391-63	Sequence 63, Appl
23	51.8	2.2	2504	4	US-09-060-610-63	Sequence 63, Appl
24	51.8	2.2	2504	5	PCT-US94-10151A-63	Sequence 63, Appl
25	51	2.2	3560	1	US-08-121-713D-59	Sequence 59, Appl
26	51	2.2	3560	2	US-08-835-268-59	Sequence 59, Appl
27	51	2.2	3560	2	US-09-060-692-59	Sequence 59, Appl

QY	472	GATGTGTCAGCTTTTCCAGCAGGTTGAA-----AGACTTTGAGAGCGGC	513
DB	322	CACATAGCGAGCTTTACTTTTAGCCCAAGATGAGGCCGGAATGATGCACTCTCGAGGATGGC	381
QY	514	CGGGGGAATGTCCTTTTGTAGCCAGCTCAACGGTCACAGCTGTAAATGGCTGGGGGGCTC	573
DB	382	AAGGGTCATTGTCTCTTTGACCCCAACTCAAGTCCACGGCTCTGGTGGTGTAGTGGTAG	441
QY	574	CTCTACACCGCCACTGTGAAGAACTTCTCGGGACTGAGCCCATCATCTCCGAGCTGTG	633
DB	442	CTGTACACTGGAACAGTCAGTAGCTTCCAGGGAACGACCCAGCCATTCCCG-----G	495
QY	634	GGTCGAGCTGAGGACTGGATTGGAACAGAGACCTGTTCATCCTGGGCTTAATGTCCAGCC	693
DB	496	AGCCAGAGTTCCCGCCCCACAGACTGAGAGCTCCCTCAACTGGCTTACAAGACCCCTGCC	555
QY	694	TTTCTGCGACGATGTCCTGAGCCAGCTGAGTGGGGGATGAGATGAGAGCAGATGAA	753
DB	556	TTTGTGCGCTGGGTAGTCCCGGAGAGCCTGGGAGCCCTAGGTGTGATGATGATGAAG	615
QY	754	ATCTTTTTTTTCTTACGGAGACCTCCGAGTGTGTGACTTCTTATGAGCCATCAAGGTC	813
DB	616	ATCTACTTCTTCTTACGAGAGCGGGCCAGGAGTTTGAGTTCTTTGAGAACACCATCGTG	675
QY	814	CCAAGATGGCCGAGTGTGTGGGGGACCTTGGGGGAGGAAAGACCCCTTCACGACAGA	873
DB	676	TCCCGAGTTGCCCGAGTCTTAAGGGCGATGAGGGTGGAGAGGGGTGTTCAGCAACGC	735
QY	874	TGGACGACGTTCTGAAGGCTGACCTGCTGTGCCAGGGCCGAGAGATGCCGGGCTCC	933
DB	736	TGGACCTCTTCTCAAGGCTGAGTCTGTGTCTCCGGCCTGATGATGCTTTCCTTT	795
QY	934	GGGGTCTCGAGGCTATGGCAGAGCTTCGGCCTCAGCCT---GGAGCGGGAACCCCATC	990
DB	796	AACGTGCTACAAGATGCTTTCACCTCGAACCCCAACCTTCAGGATTTGGGSCAAGACCTT	855
QY	991	TTTTATGGGATCTTTCTCTCCAGTGGGAAGGAGCTGCCAT-----CTCTGTGTGTGT	1044
DB	856	TCATCGGGGTCTTTACCTCCAGTGGCAGAGGGACACAGAAAGCTCTGCCATCTGC	915
QY	1045	GCCTTCGAGCCCAAGACATCCGGGAGTCTGTAATGGTCCCTTTAGAGAGCTTAAACAT	1104
DB	916	GTCTTCCACCATGAATGATGTGCAGAAGCCCTTTGACGGCCTGTACAGAAGTAAACAGA	975
QY	1105	GACTGCAACAGGGAGTGCCTGTCTATGGACAAGAGTGGCCCGAGCCAGACTGGAGAG	1164
DB	976	GAGACACAGAGTG---GTATACCGAGACCCAGAGTGGCCACACGCGCGCGGAGCG	1032
QY	1165	TGATCGCCCAACACATGAAGCTCCAGCAGTTTGGATCCTCACTCTCCCTGCCAGACCGC	1224
DB	1033	TGCATTACCAACAGTGGCCGGGAACGAAGATCACTGTCTCCCTGCACTGCCAGACCCGA	1092
QY	1225	GTGCTCACCTTTATCAGAGACCACTCTCATGGACAGGCCGCTGTTCGGGCTGACGGC	1284
DB	1093	GTGCTGAATCTCTCAAGGATCACTTCTTGATGGATGGGAGTGCC-----CGAGT	1143
QY	1285	GGCCCCCTGTGTGCTACTACAGATACAGCCCTATCTCAGAGTCTGTGGCCCCACAGGGTGACC	1344
DB	1144	CGCTGTGTGTGTGCAGCCCGAGAGCCGCTACACAGCTGTGGCTGTGACCGCTGTGCCT	1203
QY	1345	AGCCTTCACGGGAAGAATATGAGTCTCTACTCTGGGACAGAGATGGACACCTCCAC	1404
DB	1204	GGCTGCACAGCACT---TAIGATGTCCTATTCTTGGGCACTGGTATGGCGCCCTGCAC	1260
QY	1405	CGGGCTGTGCGCATTTGGAGCTCAGCTCAGTGTCTTGGAGGATCTGGCCTTGTTCAGAA	1464
DB	1261	AAAGCAGTAGCCCTGAGTCCAGAGTCCACATCATTTGAGGAGCTGCAGATCTTCCCTCAA	1320
QY	1465	CCACAGCGGTTGAGAGCATGAATGTACCAAGATTTGGCTCTCTGTGTGG-----CTCC	1518
DB	1321	GGACGCTGTGCAGAACCTGCTCTTTGGACAGCCATGGGGAGCTGTGTATGCTCTCTCC	1380

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QY 1519 CATACTGAGGTGACACAAGTGAACACAGCAACTGTGGCGCTCTCCAGAGCTGCTCGGAG 1578
Db 1381 CATTCGGGGTGGTGTGCAAGTGCCTGAGCCCAACTGCAGCCTGTACCCAACCTGTGGAGAC 1440
QY 1579 TGTATCTCTGGCCAGGACCCCGTGTGCGCCTGGA 1612
Db 1441 TGCCTCTGGCTCGAGACCCCTACTGCGCCTGGA 1474

RESULT 2
US-08-556-422A-1
; Sequence 1, Application US/08556422A
; Patent No. 6576754
; GENERAL INFORMATION:
; APPLICANT: HALL, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim L.
; APPLICANT: BOUSSIOTIS, Vassiliki
; APPLICANT: NADLER, Lee M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DEN-005CPA2
; CURRENT APPLICATION NUMBER: US/08/556,422A
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4157
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (88) ... (2673)
US-08-556-422A-1

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Query Match	9.2%;	Score 215.2;	DB 4;	Length 4157;
Best Local Similarity	48.9%;	pred. No. 1.1e-48;		
Matches	747;	Conservative 0;	Mismatches 33;	Gaps 5;
Qy	136	CCGAGAACCTCGCTGCCCATCTCGAGGCTGACTCCTATCTCAACCCGGTTTGCAGCGTCT	195	
Db	163	CCCATACCCGGATCACTCTGGGAGCAGAGAGGTGCACCTGGTGCGAGTTTTCATGAGCCA	222	
Qy	196	CATACGTACAAATTACTCTGCTCTCTTGTGTGGATCTGCCTCCCAACACACTTTAGTCCGGT	255	
Db	223	GACATCTACAACTACTCAGCCTTCTGCTGAGCGAGGACAGGACACCTTGTACATAGT	282	
Qy	256	GCAGGGATAGCATCTTCGCTTTTAAACCTGCCCTTCTCTGGGGAAGAACCCCGAAGATC	315	
Db	283	GCCCGGAGCGCGTCTTTCGCTGTGAAGGCACTCAACATCTCCGAGAAGCAGCATGAGGTG	342	
Qy	316	GACTGGATGTPACCTGAGACTCAGACAGAACTGCAGGAAGAAGCAAG--AAAGAG	372	
Db	343	TATTGGAAAGTCTCAGAAAGACAAAAGCAAAATGTGCAGAAAAGGGAAATCAAAACAG	402	
Qy	373	GACGAATGTCACAAATTTTCCAGATTCTCGCCATTGTCAATGCTCTCACTCCTCACG	432	
Db	403	ACAGAGTGCCTCACTACATCCGGGTGCTGCAGCCACTCAGCGCCACTTCCCTTTACGTG	462	
Qy	433	TGCGGCACCTTCGCTTTTGATCCGAAGTCGGGGGTATTGATGTGCCAGTTTCCAGCAG	492	
Db	463	TGTGGGACCAACGCATTCCAGCCGGCGTGTGACCCACCTGAACTTTAAGCTTTTAAAGTTT	522	
Qy	493	GTTCAAAGACTTGAGAGCGCGCGGGGAAATGTCTTTTGAGCCAGCTCAACGCTCAGCA	552	
Db	523	CTGGGGAAAATGAAGATGGCAAGGAAGATGTCCCTTTTGACCCAGCACACAGCTACACA	582	
Qy	553	GCTGTAATGGCTGGGGCGTCTCTCACACGCCACTGTGAAGAATCTCTCGGGACTCGAG	612	
Db	583	TCCGTCATGGTTGATGAGAACTTTATTTCGGGACGTCGTATATTTTTTGGGAAGTGAA	642	
Qy	613	CCCATATCTCCCGAGCTGTGGGTGAGACTGAGGACTCGGATTCGAACAGAGACCTTGTCA	672	
Db	643	CCCATATCTCCCGAAATTTCTCCACAGTCTCTGAGGACAGAAATATGCAATCC-----	697	

QY	673	TCCTGGCTTAAATGCTCCAGCGTTTGTGTCGACAGCTAATGATCTCTGAGCCGACGCTGAGTGGGGG	732
Db	698	-TTTGGCTGAACGAGCCTAGTTTTCGTGTTTTCGTGACGTGATCCGAAAGCCGACAGCAGC	756
QY	733	GATGAAGATGGAGACGATGAATCTTTTTCACGGAGACCTCCCGAGTGTGTGGAC	792
Db	757	CCGACGCGGAGGATGACAGGCTACTTCTTTCACGGAGGTGCTGTGGAGATGAG	816
QY	793	TCCTATGAGCGCATCAAGGTCCTCAAGAGTGGCCGAGTGTGTGGGGGACCTTTGGGGC	852
Db	817	TTTGTGTTCAGGGTGTCTATCCACGGATAGCAAGAGTGTGCAAGGGGACACGAGCGCG	876
QY	853	AGGAAGACCCCTCAGCAGAGATGACAGACGTTTCTGAAGCTGACCTGCTGCCAGGG	912
Db	877	CTGAGGACCTTGCAGAAAGAAATGACCTCTCTGAAAGCCGACATCTGCTCCCGG	936
QY	913	CCGAGCATGGCCGGGCTCCGGGGTTCTCGAGGCTATGCGAGAGCTTCGGCCCTCAGCCT	972
Db	937	CCAGACAGCGCTTGGTCTTCAATGTGCTCGGGATGCTTCGTGCTCAGGTC--CCCG	993
QY	973	GGAGCGGAACCCCATCTTTTATGGGATCTTTTCTCCAGTGGGAGAGCTGCCATC	1032
Db	994	GGCCTGAAGGTGCCGTGTGTTCTATGCACTCTTCAACCCACAGCTGAACAAGTGGGGCTG	1053
QY	1033	TCCTGCTGTGTGTC-----TTCCGACCCCAAGACATCCGGGCGAGTCTGAATGTT	1083
Db	1054	TCGSCAGTGTGCGCTACAACCTGTCACAGCGGAGGAGTCTTCTCCACGGGAGTAC	1113
QY	1084	CCCTTTAGAGAGCTAAACATGACTGCAACAGGGGAGCTGCCTGTCTATGGACAACGAGGTG	1143
Db	1114	ATCGAGAGCACCAAGTGGAGCAGTCCACACCAAGTGGTGGGCTATAATGCCGGTA	1173
QY	1144	CCCAGCGCCAGAGCTGGAGAGTGATCGCCCAACAACATGAAGTCCAGCAGTTTGGATCC	1203
Db	1174	CCCAAGCGCGGCTGGAGGCTGATCGACAGGCGGCGGCGGCAACTACACCAGC	1233
QY	1204	TCACTCTCCCTGGCAGACCGGCTGCACCTTTATCAGAGCACCCCTCTCATGGACAGG	1263
Db	1234	TCCTTGAATTTGGCAGACAAGCGCTGCAGTTTCGTTAAAGACCAACCTTTGATGGATGAC	1293
QY	1264	CCGCTGTTCCGGCTGACGGCGGCCCTCTGCTGCTACTACAGTACAGGCTATCTCAGA	1323
Db	1294	TCGGTAACCCCAATGACAACAGCCCGAGTTAATCAAGAAGATGTGAACATACACCAG	1353
QY	1324	GTGCTGCCCCACAGGTTGACACCTCTCAGGGAAGAATATGACGTGCTCTACCTGGGG	1383
Db	1354	ATCGTGTGTGACCGGACCCAGGCCCTGGATGGGAGTCTATGATGTCATGTTGTGACG	1413
QY	1384	ACAGAGATGGACACCTCCACCGGGCTGTGCGCATTTGGAGCTCAGCTGATGCTTTGGAG	1443
Db	1414	ACAGCGGGGAGCTGTGCACAAGCCATCAGGCTCGAGCACGCTGTTCACATCATCGAG	1473
QY	1444	GATCTGGCCCTGTGTTCCAGAACACAGCCGGTTGAGAGCATGAATGTGA-----	1493
Db	1474	GAGACCCAGCTCTTCCAGGACTTTGAGCCAGTCCAGACCTGCTGCTGCTTCAAGAAG	1533
QY	1494	--CCACGATTGGCTCTCTGGTGGGCTCCCATCTACTGAGGTGACAGAAGTGAACACCGAAC	1551
Db	1534	GGCAACAGGTTTGTCTATGCTGGCTCTAACTCGGGGTGGTTCGAGGCCCGCTGGCCTTC	1593
QY	1552	TGTGGCCGCTCTCAGAGCTGCTCGGAGTGTATCTTGGCCCGAGGACCCGCTGTCGGCTGG	1611
Db	1594	TGTGGGAAGCAGGCACCTCGGAGGACTGTGCTGGCGCGGAGCCCTACTCGGCTGG	1653
QY	1612	AGCTTCGGGCTGTGATGCTGTGTGGGCC	1639
Db	1654	AGCCGCCACAGCAGCTCGGTGGGTC	1681

RESULT 3

RESOLUTION 3
US-09-0777-940A-3

US 03 077 340A-3
; Sequence 3, Application US/09077940A

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; Patent No. 6576441
;
; GENERAL INFORMATION:
;
; APPLICANT: KIMURA, Toru et al.
;
; TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE SAME
;
; FILE REFERENCE: 0020-4426P
;
; CURRENT APPLICATION NUMBER: US/09/077,940A
;
; CURRENT FILING DATE: 1998-06-05
;
; NUMBER OF SEQ ID NOS: 20
;
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 3
;
; LENGTH: 3524
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
;
; FEATURE:
;
; NAME/KEY: 5'UTR
;
; LOCATION: (1)..(38)
;
; OTHER INFORMATION:
;
; NAME/KEY: 3'UTR
;
; LOCATION: (2706)..(3524)
;
; OTHER INFORMATION:
;
; NAME/KEY: CDS
;
; LOCATION: (39)..(2702)
;
; OTHER INFORMATION:
;
; US-09-077-940A-3

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Query Match	4.08;	Score 94.2;	DB 4;	Length 3524;
Best Local Similarity	47.6%;	Pred. No. 1e-15;		
Matches 448;	Conservative 0;	Mismatches 448;	Indels 45;	Gaps 4;
Qy	338	ACACACAGAACTGCAGGAAGAAAGGCGCAAGAAAGAGGACGAATGTCACAAATTTTATCCAGA	397	
Db	373	ACATAAAGCTGTGTCGGATGAAGGCAAAACAGGAGGCGAGTGTGCGAAACTTCGTAAAGG	432	
Qy	398	TTCTCGGCATTGTCAATGCCTCTCACCTCTCAGCTGCGGCACCTTCGCTTTTGTATCCGA	457	
Db	433	TGCTGCTCTTCGGGACAGTCCACGCTCTTTGTGTCGGTTTCAACGCCCTTCNACCCGG	492	
Qy	458	AGTCGGGGTTATTGATGTGTCCAGTTTCCAGCAGGTTGAAAGACTTTGAGAGCGCGCGG	517	
Db	493	TGTGCGCAACTACAGCATAGACACCTTCGACGCCGTGCGGAGACAACATCAGCGGTATGG	552	
Qy	518	GGAATATGCTTTTGAAGCCAGCTCAACGGTTCAGCAGCTGTAAATGGCTGGGGGGTCTCT	577	
Db	553	CCCGCTCCGCGTAGACGCCCAAGCACGCCAAATGTTGCCCTCTTCTCTGACGGGATGCTCT	612	
Qy	578	ACACCGCACTGTCAAGAACTTCTCTGGGGACTGAGCCCATCATCTCCCGAGCTGTGGGTC	637	
Db	613	TCACAGCTATGTTTACCAGCTTCTTACGCCATTGATGCTGTCTATCCGCGAGCCTCGGGG	672	
Qy	638	GAGCTGAGGACTGGATTTCGAACAGAGACCTTGTTCATCCTCGCTCTTAATGCTCCAGCCTTTG	697	
Db	673	ACAGGCCACCCTCGCGCACCGTGAAACATGACTCCAAGTGGTTCAAAGACCTTACTTTG	732	
Qy	698	TCGACGATATGGTCTTGAGCCAGCTGAGTGGGGGGATGAAGTGGAGACGATGAANAATCT	757	
Db	733	TCCATCGGTGGAGTGGGGGAGCCATG-----TCT	762	
Qy	758	TTTTTTTCTTCACGGAGACCTCCCGAGTGTGGACTCTATGAGCGCATCAAGGTCCCAA	817	
Db	763	ACTTCTTTCTCCGGGAGATTGCGATGAGTGTAACTACCTGGAGAGGTCGTGTGTC	822	
Qy	818	GAGTGGCCCGAGTGTGTGCGGGGACCTTGGGGCGAGGAACCC-----CTTCAGCAGAGAT	874	
Db	823	CGGTGGCCCGAGTGTGCAAGACGCTGGGAGGCTCCCCCGGCTCTCGAAGACGAGT	882	
Qy	875	GGACAGCTTTCTGAAGGCTGACCTGCTGTGCCAGGCGCCGAGCATGGCCGGCCCTCCG	934	
Db	883	GGACGTCCTTCCGTAAGCGCGGCTCAACTGCTGTGTACCCGGAGACTCCCAATTTCTACT	942	
Qy	935	GGGTTCGACAGGCTATGGCAGAGTTCGCGCCTCAGCCTTGAGCGGGGAACCCCAATCTTTT	994	
Db	943	TCAACGTGCTG-----CAGGCTGTACGGCGGTGGTTCAGCCTTCGGGGCGCGCCCTGTGTC	999	


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: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/121,713
: FILING DATE: 13-SEP-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Osman, Richard A.
: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: B94-002-1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415)343-4341
: TELEFAX: (415) 343-4342
: TELEX:
: INFORMATION FOR SEQ ID NO: 57:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2854 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 451..2640
: US-08-833-391-57

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Query Match	2.98;	Score 66.6;	DB 3;	Length 2854;
Best Local Similarity	47.3%;	Pred. No. 3.2e-08;		
Matches 269;	Conservative 0;	Mismatches 294;	Indels 6;	Gaps 2;
QY	66	GC	CGCTGCTCGCTGCTGCTGCTGCTGCGGATACTAAGCGCCCGGCTGCGCGCGCGTCCC	125
Db				
QY	453	GC	GGCGGCGGCTGCTGGCGGCTGCGGCGCTGCTTTGGGTGGCGCTGCACCGCCCGCGATG	512
Db				
QY	126	CC	GCTCAGTGCCCAAGAACCTTCGCTGCCCATCTCCGAGGCTGACTCCTATCTCACCCCGGTT	185
Db				
QY	513	GG	TCAACGACGCTCAGCGCCCAAGATGTAGCTCCAGTTCGGTGAGGAACGGGTGCAACGCTT	572
Db				
QY	186	TG	CAGCGCTCTCATCGTACATAATTA	245
Db				
QY	573	CT	TGGGCAATGAATCGCAACAAAGACCACTTCAAGCTGCTGGGAAGACACACAACCTCGCT	632
Db				
QY	246	TT	ACGTGCGGTGCACGGGATAGCATCTTCGGCTTTAAACCTCC	302
Db				
QY	633	CC	TGCTAGGAGCTAGGAACATCGCTACATATCAGCCTTCGAGACCTCACAAATTCAC	692
Db				
QY	303	AC	CCCGAAGATCGACTGGATGGTACCTGAGACTCACAGACAGAACTGCGAGGAAGAAGG	362
Db				
QY	693	CG	AGCAGAGATCGAGTGGCACTCGTCAGGTGCCCATCGCGAGCTCTGCTACCTCAAGGG	752
Db				
QY	363	CA	AGAAGAGGACGAATGTCACAATTTATTCAGATTCTCGCCATTGTCATGCTCTCA	422
Db				
QY	753	GA	GTCAGAGACGACTGCCAAGACTACATCCGAGTCTCGGGAATTCACGATGACCG	812
Db				
QY	423	CT	CTCTACGTCGGCACCTTCGCTTTGATCCGAAGTGC	482
Db				
QY	813	CG	TACTCATCTCGGTCAGAACGCTATAAGCCACTATGTCGCACCTACGCCCTCAAGGA	872
Db				
QY	483	TT	TCCAGCAGGTT	539
Db				
QY	873	TG	GAGATTATGTTGAGAGAAAGAAATGAGGGAAGAGGATGTGCCCATTTGACCCCTGA	932
Db				
QY	540	TC	AACGGTTCAGCAGCTGTTAATGGCTGGGGCGTCTCTACACCGCCACTCTGGAAGAACTT	599
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QY	933	CC	ACAACAGCACTGCAATATACAGTGAAGGACAAATGCTACTCAGACACACTGGCAGACTT	992
Db				
QY	600	CT	TGGGACTGAGCCCAATCATCTCCGAG	628
Db				
QY	993	CT	CTGGAACCTGACCCCTCTCATATACCGCG	1021
Db				

RESULT 9
US-09-060-610-57
; Sequence 57, Application US/09060610
; Patent No. 634544
; GENERAL INFORMATION:

APPLICANT: Goodman, Corey S.
 APPLICANT: Kolodkin, Alex L.
 APPLICANT: Matthes, David
 APPLICANT: Bentley, David R.
 APPLICANT: O'Connor, Timothy
 TITLE OF INVENTION: The Semaphorin Gene Family
 NUMBER OF SEQUENCES: 100
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 268 Bush Street, Suite 3200
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/060,610
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/835,268
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Osman, Richard A.
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: B94-002-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415)343-4341
 TELEFAX: (415) 343-4342
 TELEX:
 INFORMATION FOR SEQ ID NO: 57:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2854 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 451..2640
 US-09-060-610-57

	Query Match	2.9%	Score 66.6	DB 4	Length 2854		
	Best Local Similarity	47.3%	Pred. No. 3.2e-08				
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Qy	66	GC	CGCTGTCGCTGCTGCTGCTGCTGCGGATACATAAGCCGCCCGGTGTGCGGCCGCGTCCC	125			
Db	453	GC	GGCGCGCGCGCTGCTGCGCGCGCTGCTTTTGGGTGCGGTGCACGCCGCGCGCATG	512			
Qy	126	CC	GCTCAGTGC	CGCCAAACCTCGTGC	GC	CCATCTCCGAGGCTGACTCTCTCACCCGGTT	185
Db	513	GG	TCACACGCGT	CAGCCCCAAGATGATCGTCCAGTTCGGT	GAGGAACGGGTGC	CAACGCTT	572
Qy	186	TG	CAGCGTCTCATACGTACAAATTA	CTGCTCTCTCTTGTGGATCCTCGCTCC	CCACACACT	245	
Db	573	CT	GGGCAATGAATCGCACAAAGACCACTTCAAGCTGCTGG	AAGACCACTCGCT	632		
Qy	246	TT	ACGTCGGTG	CAGGGATAGCATCTTCGCTTTAA	CCCTCC	---CCTTCTCTGGGGAAG	302
Db	633	CT	CGTAGGAGCTAGGAACATCGTCTACAATATCAGCCTT	CGAGACCTC	CACAGAAATTCAC	692	
Qy	303	AC	CCCGAAGATCGACTGGATGGT	TACCTGAGAGCTCACAGACAGAACTCGAGGAAGAAGG	362		
Db	693	CG	AGCAGAGATCGAGTGGC	ACTCGT	CAGGTGCCCATCGCGAGCTCTGCTACCTCAAGGG	752	
Qy	363	CA	GAAGAAGAGGACGAATGTCACAAATTTTATTCAGAT	TCTCGCCATTTGCTCAATGCCCTCTCA	422		
Db	753	GA	AGTCAGAGGAGGAGCTGCCAGAACTACATCCGAGTCT	CGCGAAAAATTCACATGATGCCG	812		

QY	423	CCTCCTCAGGTGCGGCACCTTTCGGTTTGATCCGAAGTCGGGGTTATTGATGTGTGCCA	482
Db	813	CGTACTCATCTCGGTCAGCAACGCTATATAGCCACTATGTCGGCACTACGCCCTCAAGCA	872
QY	483	TTTTCCAGCAGGTT---GAAAGACTTTAGAGGGCGGGGGAATGTCCTTTTGGAGCCAGC	539
Db	873	TGGAGATTATGTTGTAGAGAAAGAATAAGAGGAAGAGGATTGTGCCATTTCACCCTCA	932
QY	540	TCAACGGTTCAGGACTGTATTCGCTGGGGGGTCTCTACACGGCACCTGTGAAGAACTT	599
Db	933	CCACAACAGCACTGCAATATACAGTAGGGACAATTCGTACTCAGAACAGTGGCAGACTT	992
QY	600	CTGGGGACTGAGCCCATCTCTCCGAG	628
Db	993	CTCTGGAACCTGACCTCTCATATACCGC	1021

RESULT 10

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PC-TUS94-10151A-57
; Sequence 57, Application PC/TUS9410151A
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR HOBBACH TEST ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10151A
; FILING DATE: 13-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: FP-58750-PC/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2854 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 451..2640
PC-TUS94-10151A-57

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186	QY	TCGAGGTCCTCATACGTACAAATTACTCTGTCTCTCTTGTGGATCCTGCCTCCACACACTT	245
573	Db	CCTGGGCAATGAATCGCAAGAAGCCACTTCAAGCTGCTGGAGAAGGACCACAACTCGCT	632
246	QY	TTTACGTCGGTGCACGGGATAGCATCTTCGCTTTTAAACCTCC---CCTTCCTCTGGGAAAG	302
633	Db	TTTACGTCGGTGCACGGGATAGCATCTTCGCTTTTAAACCTCC---CCTTCCTCTGGGAAAG	692
303	QY	ACCCGGAAGGATCGACTGGATGGTACCTGTGAGACTTCACAGACAGAACTGCAGGAAGAAGAG	362
693	Db	CGAGCAGAGGATTCGAGTGGGCACCTCGTCAGGTGCCATCGCGAGCTCTGCTACCTCAAGGG	752
363	QY	CAAGAAGGAGCAGGAATCTACAAATTTTATCCAGATTCTCGCCATTGCTCAATGCCTCTCA	422
753	Db	GAAGTCAGAGGACGAGTCCAGAACTACATCCGAGTCTCGCGAAATTTGACCATGACCG	812
423	QY	CTCTCTACGTCGCGCAGCTTCGCTTTTGTATCCGAAGTGGCGGGTTATTGATGTGCCAG	482
813	Db	CGTACTCATCTCGGTCAGAACGCCCTATAAGCCACTATGTCGGCAGCTACGCCCTCAAGGA	872
483	QY	TTTTCAGCAGGTT---GAAGACTTTGAGAGGGCGGGGGAATGTCTTTTGGCCAGC	539
873	Db	TGGAGATTATGTTGTAGAGAAAGAAATATGAGGGAAGAGGATTTGTCCTTTGACCCCTGA	932
540	QY	TCACGGGTACAGCAGCTGTAATGGCTGGGGGGTCTCTACACGCCCACTGCTGAAGAACTT	599
933	Db	CCACAACAGCACTGCAATATACAGTGAAGGACAAATTTGTTACTACGAACAAGTGGCAGCTT	992
600	QY	CCTGGGAGCTAGGCCCATCATCTCCGAG	628
993	Db	CTCTGGAACCTAGCCCTCTCATATACCGCG	1021

RESULT 17

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Db	525	ATATGACCCCTAAGCTGCTGACAGCATCCCTTTTAAATAGATGGAGAAATATAC	584
Qy	588	TGTGAAGAACTTCCCTGGGGACTGAGCCCATCATCTCCCGAGCTGTGGGTGAGCTGAGGA	647
Db	585	TGCAGCTGATTTATGGGCGAGACTTTGCTATCTTCGAACTCTTGGGCACCA	644
Qy	648	CTGGATTCGAACAGAGACCTTGTCTATCTGCTTAACTGCTCCAGCCCTTGTCTCAGCTAT	707
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Qy	888	GAAGGCTGACCTGTGTGCCAGGGCCCG	916
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RESULT 13
US-09-060-692-53
: Sequence 53, Application US/09060692
: Patent No. 5935865
: GENERAL INFORMATION:
: APPLICANT: Goodman, Corey S.
: APPLICANT: Kolodkin, Alex L.
: APPLICANT: Matthes, David
: APPLICANT: Bentley, David R.
: APPLICANT: O'Connor, Timothy
: TITLE OF INVENTION: The Semaphorin Gene Family
: NUMBER OF SEQUENCES: 100
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
: STREET: 268 Bush Street, Suite 3200
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/060,692
: FILING DATE:
: CLASSIFICATION: 514
: PRIOR APPLICATION NUMBER:
: APPLICATION NUMBER: US/08/121,713
: FILING DATE: 13-SEP-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Osman, Richard A.
: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: B94-002-1
: TELEPHONE: (415)343-4341
: TELEFAX: (415) 343-4342
: TELEFAX:
: INFORMATION FOR SEQ ID NO: 53:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2601 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA

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;
; NAME/KEY: CDS
; LOCATION: 16..2331
US-09-060-692-53

Query Match      2.68; Score 60.6; DB 2; Length 2601;
Best Local Similarity 47.9; Pred. No. 1.3e-06;
Matches 359; Conservative 0; Mismatches 354; Indels 36; Gaps 5;

QY 192 GTCTCATACGTACAAATTACTCTGCTCTCCTTGTGGATCCCTCCACACACTTTACGT 251
DB 168 GCCCAACAGCTCCAGTTTATCATACCTTCCCTTTTGGATGAGAACGGAGTAGGCTGTATGT 227
QY 252 CGGTGTCACGGGATAGCATCTTCGCTTTAAACCCCTCCCTTCTCTGGGAAAGACCCCGAAG 311
DB 228 TGGAGCAAGAGATCACATAATT--TTTATTCGACCTGGTTTAATATCAAGGATTTTCAAAA 284
QY 312 GATCGACTGGATGTACTGAGACTACAGACAGAACTGCAGGAGAAAGAGGCA---AGAA 368
DB 285 GATTGTGTGCCAGTATCTTTACACCAAGAGAGATGAATGCAAGTGGGCTGGAAAAGACAT 344
QY 369 AGAGGAGCAATGTACAAATTTTATCCAGATTCGCGCATTTGCAATGSCCTCTCACCTCCT 428
DB 345 CCTGAAAGAATGTGCTTAATTCATCAAGGTACTTTAAGGCATTAATACAGACTCACCTTGTA 404
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QY 489 GCAGGTTGAAAGACTTTGAG-----AGCGCGGGGGGAAATGTGTC 527
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DB 645 AATCAGGACAGAGCAGCATGATTCAGGTGGCTCAATGATCCAAAGTT-----CATTT 696
QY 708 GGTCTCTAGCCAGCTCAGTGGGGGATGAAGATGGAGAGCATGAATCTTTTTTTTCTTT 767
DB 697 AGTGCCCACTCATCTCAG--AGAGTGACAATCTCTGAAGATGACAAAGTATACTTTTTTCTT 755
QY 768 CACGGAGACCTCCCGAGTGTGACCTCTATGAGCGCATCAAGGTCCCAAGAGCTGGCCCG 827
DB 756 CCGTGAATATGCAATAGATGGAGAACACTCTGAAAAGACTACTCAGCTAGATAGTCA 815
QY 828 AGTGTGTGGGGGAGCTTTGGGGGAGAGAACCCCTTCAGCAGAGATGGACGACGTTTCT 887
DB 816 GATATGCAAGAATGACTTTTGGAGGGCACAGAGTCTGGTGAATAAATGGACAACATTCCT 875
QY 888 GAAGGCTGACCTGCTGTGCCCAGGGCCG 916
DB 876 CAAAGCTCGTCTGATTGCTCAGTGCAG 904

RESULT 14
US-08-833-391-53
; Sequence 53, Application US/08833391
; Patent No. 6013781
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family

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Result No.	Query 8				ID	Description
	Score	Match	Length	DB		
1	1626	69.8	2893	11	US-09-808-665A-1	Sequence
2	1626	69.8	2894	11	US-09-808-665A-3	Sequence
3	654	28.1	799	11	US-09-808-665A-5	Sequence
4	567.6	24.4	928	14	US-10-188-246-13	Sequence
5	527.4	22.6	777	14	US-10-188-246-15	Sequence
6	251.8	10.8	3293	14	US-10-149-819-25	Sequence
7	248.6	10.7	2155	13	US-10-003-152-11	Sequence
8	248.6	10.7	2155	14	US-10-002-050-11	Sequence
9	248.6	10.7	2155	14	US-10-002-304-11	Sequence
10	248.6	10.7	2156	13	US-10-003-152-21	Sequence
11	248.6	10.7	2156	14	US-10-002-050-21	Sequence
12	248.6	10.7	2156	14	US-10-002-304-21	Sequence
13	248.6	10.7	2284	13	US-10-003-152-13	Sequence
14	248.6	10.7	2284	14	US-10-002-050-13	Sequence
15	248.6	10.7	2284	14	US-10-002-304-13	Sequence
16	247	10.6	3781	11	US-09-946-374-252	Sequence

QY	121	GTCCCCCGCTCAGTGGCCCGAGAACCTTCGCTGCCCATCTCCGAGGCTGACTCTATCTCACC	180
DB	215	GTCCCCCGCTCGGTGCCAGAACCTTCGCTTCCAATCTCTGAGGCTGACTCCTGTCTCACC	274
QY	181	CGGTTGCGAGCGTCTCATACGTACAGTACAAATTACTCTGCTCTCCCTTGTGGATCTCGCTCCACC	240
DB	275	CGGTTGCGAGTCCCTCACACATACANTTACTCTGTCTCTCTTGTGGATCTCGCTCCACC	334
QY	241	ACACTTTACGTCGGGTGCACGGATAGCATCTTCGCTTTAACCCCTCCCTCTCTCTGGGAA	300
DB	335	ACACTTTATGTTGGCGCCGGACACCATCTTCGCTTTATCCCTGCCCTCTCAGGGGAG	394
QY	301	AGACCCCAAGGATCGACTGATGGTACTGAGACTCACACACAGAACTCGCAGGAAGAAA	360
DB	395	AGACCCCGAGATTGACTGGATGGTCTCGAGGCTACAGACAGAACTGTAGGAAGAAA	454
QY	361	GCCAAAGAAAGAGGACGAATGTACAAATTTATCCAGATTCTCGCCATTGTCAATGCCCTCT	420
DB	455	GGCAGAAAGAG-----	466
QY	421	CACCTCTCACGTGCGGCACCTTCGCTTTTGATCCGAAGTCGGGGTTATTGATGTGTCC	480
DB	467	-----GATGTGTCC	475
QY	481	AGTTTCCAGCAGGTTGAAGACATTGACAGCGCGCGGGGAAATGTCTCTTTTGAGCCAGCT	540
DB	476	AGGTTTCCAGCAGGTTGAAGACTTGAAGTGGCGCGGGGAAATGTCTCTTTTGAGCCAGCT	535
QY	541	CAACGGTCAAGCAGCTGTAAATGGCTGGGGCGCTCTCTACACCGCACCTGTCAAGAACATTC	600
DB	536	CAGCGTCAAGCAGCTGTAAATGGCTGGGGGGTCTCTATGCTGCCACTGTGAAAAACTATC	595
QY	601	CTGGGACTGAGCCCATCATCTCCGAGCTGTGGGTGAGCTGAGGACTGGATTCGAACA	660
DB	596	CTGGGAGCGAGCAATTTATCACCAGAGCAGTGGGTGTCGCCGAGGACTGGATTCGGACA	655
QY	661	GAGACCTTGTCATCTCTGGCTTAATGCTCCAGCCCTTTGTCGAGACTATGGTCTCAGGCCA	720
DB	656	GATACCTTGGCTTCTTGCTGTAAGCGCCCGAGCCCTTGTGCGAGCGGTGGCTTGAGGCCA	715
QY	721	GCTGAGTGGGGGATGAAGATGGAGACCATGAAATCTTTTCTTTTCTCACGGACACCTCC	780
DB	716	GCCGAATGGGGGATGAAGATGGAGACGACGAATCTACTTCTCTTTACGGACACTTCC	775
QY	781	CGAGTGTGGACTCCTATGAGCGCATCAAGTCCCAAGTGGCCCCGAGTGTGTGCGGGG	840
DB	776	CGAGCATTTGACTCATAGAGCGCATTAAGTCCACGGGTGGCCCGTGTGTGTCGGGG	835
QY	841	GACCTTGGGGCAGGAACCCCTTCACGAGATGGACGCTTCTGAAGGCTGACTCG	900
DB	836	GACCTCGGGGCCGGAAGACCCTCCAGCAGATGGACGAGCTTTTGAAGCTGAGCTG	895
QY	901	CTGTGCCAGGGCCGAGCATGGCCGGGCTCCGGGGTCTGCAAGGCTATGGCAGAGCTT	960
DB	896	CTCTGTCCAGGGCTGAGCATGGCCGGCCCTCCAGTGTCTGTCAGGATGTGTCTGCTCT	955
QY	961	CGGGCTCAGCCTGAGGCGGGAACCCCACTTTTATGGGATCTTTTCTCCCACTGGGAA	1020
DB	956	CGACTGAGCTTGGGGCAGGAGCTCCCATCTTTTATGGCATCTTTCTTCTCCCACTGGGAG	1015
QY	1021	GGAGCTGCCATCTCTGCTGTGTGCTCTCGACCCCAAGACATCCGGGAGTGTCTCAAT	1080
DB	1016	GGGGCTACTATCTCTGCTGTCTGTGCTCTCGACCAAGACATTCGGCAGTGTCTCAAT	1075
QY	1081	GGTCCCTTTAGAGAGCTAAAACATGACTGCAACAGGGGAGTGCCTGTCTATGGCAACGAG	1140
DB	1076	GGTCCCTTCAGAGAACTAAAACATGACTGCAACAGAGAGTGCCTGTCTGGCAGATGAT	1135
QY	1141	GTGCCCCAGCCAGACCTGGAGAGTGATCGCCAAACAACTGAAGCTCCAGCAGTTTGA	1200
DB	1136	GTGCCCCAGCCAGACCTGGAGAGTGATCACCACCAACATGAAGCTCCGGCAGTTTGGC	1195

QY	1201	TCCTCACTCTCCCTGCCAGACCGCGTGGTCACTTTATCAGAGACCACCTCTCATGGAC	1260
Db	1196	TCACTCTCTCCCTGCCTGACCGGTACTCACCTTCTATCCGGGACCAACCACCATGGAC	1255
QY	1261	AGGCCCGTGTTCCCGCGCTGACGGCGGCCCGCTGCTGGTCACTACAGATACAGCTATCTC	1320
Db	1256	AGGCCAGTGTTTCCAGCTGATGGCCACCCCCTGCTGTCTACTACAGATACAGGCTATCTC	1315
QY	1321	AGAGTCGTGGCCACACAGGGTGACACAGCTCTCAGGGAAAGAATATAGCTGCTTACCTG	1380
Db	1316	AGAGTCGTGGCCACACAGGGTGACACAGCTCTCAGGGAAAGATATGATGTGCTTACCTG	1375
QY	1381	GGGACAGAGTAGGACACCTCCACC GGCGTGTGGCCATTGGAGCTCAGCTCAGTGTCTTG	1440
Db	1376	GGGACAGAGTAGGACACCTCCACC GAGCAGTGGGATCGGAGTCAAGCTCAGCTCAGCTTCTT	1435
QY	1441	GAGGATCTGGCGTTGTTCCCAAGAACCAACAGCCGGTTGAGAGCATGAANAATTGTACCAGGAT	1500
Db	1436	GAAGATCTGGCGTTATTTCCCAAGACCCAACGCCAGTTTGAGAACATGAANAATTGTACCACAGC	1495
QY	1501	TGGCTCCCTGGTGGCTCCCACTACTGAGGTGACACAAGTGAACACCACTCACTGTGGCCGT	1560
Db	1496	TGGCTCCCTGGTGGCTCCCGTACTGAGGTGNACACAGTGAATACACCACTGTGGCCGT	1555
QY	1561	CTCCAGAGCTGCTCGGAGTGTATCTTGGCCCCAGGACCCCGTGTGGCGCTGGAGCTTCCCGG	1620
Db	1556	CTCCAGAGCTGCTCAGAGTGCATCTTGGCCCCAGGACCCAGTCTGTGCTGGAGCTTCCCGG	1615
QY	1621	CTTGATGCTTGTGTGGCCACCGCCGGGAGGACCGCGGGATGGTTCAAGATATAGAGTCA	1680
Db	1616	CTGGATGAGTGTGTGGCCCATGCCC GGCGGAGCCCGAGGGTTGGTCCCAAGACATAGAGTCA	1675
QY	1681	GCGGATGTCCTCTCTTTGTGTCCAAAAGAACCTTGGAGAACATCCCGTGTGTTGAAGTT	1740
Db	1676	GCAGATGTCCTCTTGTGTCTTAAGAGCTTGGAGAACGTCCAGTAGTGTGTTGAAGTT	1735
QY	1741	CCGCTGGCTACTGTGGCCACAGTGGTCTTGCCCATGTTTCCCCCAAGTGTCTGCTGGGCAATCC	1800
Db	1736	CCCCTGGCTACAGCTGCGCATGTGGTCTTGCCATGTTTCCCAAGCTCAGCATGGGCAATCC	1795
QY	1801	TGTTGTGGCACACAGCCCGCATGGAGTCACTTGGCGTCACTCCC CGGAGGGATGACATAGAG	1860
Db	1796	TGTTGTGGCACCAACGACGTTGGAGTGTACTGTCACTACCCCGCGGGATGAGCATGGAG	1855
QY	1861	GTGTTGTGACCCACAGGGCCATGGGGGCTTATGTCTTGGAGTGTCAAGGAGGTGGAGCC	1920
Db	1856	GTGTTGTGACCCACAGGGCCATGGGGGCTTATGTCTTGGAGTGTCAAGGAGGTGGGGCA	1915
QY	1921	GCCGCGGTGGTGGCTTATAGCTTGGGTGGGGCAGCCAGCGGGGACCCCTCAAACCGG	1980
Db	1916	GCCCATGTGGTAGCAGCTTACAGCTTGGTATGGGGCAGCCAGCAGATGCTCCGAGCCCGG	1975
QY	1981	GCCACACCGTTGTGGGGGCTGGATGGTTGGCTTTCTCTGGGTGTTCTTGCAGCATCC	2040
Db	1976	GCCACACAC --- AGTGGGGGGGGGACTGGCTGGCTTCTTCTTGGGGATCTTCGCAGCATCC	2032
QY	2041	CTCACTCTCTCTGATTGTGTCGCGTFCAGCAGCTGCGGCGACAGAGGGAGCTTCATGCT	2100
Db	2033	CTGACTCTCATCTGATTGGTCGGCTFCACAGCGGCGGCGACAGAGGGAACTTCCTGGCT	2092
QY	2101	AGAGACAAGGTGGGCTTATAGTCTGGGGGCTTCCACCTTCTGGGACCAACAAGCTATAGTCAG	2160
Db	2093	AGAGACAAGGTGGSCCTGGACCTGGGGGCTCCACCTTCTGGGACCAACAAGCTACAGCCAA	2152
QY	2161	GACCTCTCTCTCTTCGCCCTGAAGATGAACGGCTGGCCCTGGGTAAAGCGGGG	2220
Db	2153	GACCTCTCTCTCTCTCTGAAGATGAGCGGTTGGCGCTGGCCCTGGCCAAAGAGGGG	2212
QY	2221	AGTGGTTTTGGTGGCTTCCCTCCACCTTCTCTCTGGATTCCTTGGCCAAAGCGGCCAC	2280
Db	2213	AGTGGCTTTGGTGGATTTCTCACCACCTTCTCTCTGTATCTTGTGCCAAGCGGCCAC	2272
QY	2281	ATCCGGCTCACTGGGGCGGCTCTTAGCCACAGCTGTGATGAGACCTTCCATCTATA2330	


```

; APPLICANT: Boldog, Ferenc,
; APPLICANT: Casman, Stacie,
; APPLICANT: Edinger, Shlomit,
; APPLICANT: Gerlach, Valerie,
; APPLICANT: Gorman, Linda,
; APPLICANT: Li, Li,
; APPLICANT: Malyankar, Uriel,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Peyman, John,
; APPLICANT: Shenoy, Suresh,
; APPLICANT: Shimkets, Richard,
; APPLICANT: Vernet, Corine A. M.,
; APPLICANT: Voss, Edward
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-397B US
; CURRENT APPLICATION NUMBER: US/10/188,246
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 60/303046
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/304502
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/305011
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/306085
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 60/326981
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/360923
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/363636
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/373063
; PRIOR FILING DATE: 2002-04-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Custom
; SEQ ID NO 13
; LENGTH: 928
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (55)..(922)
; US-10-188-246-13

Query Match          24.4%; Score 567.6; DB 14; Length 928;
Best Local Similarity 86.7%; Pred. No: 4e-157;
Matches 643; Conservative 0; Mismatches 84; Indels 15; Gaps 1;

Qy 1 ATGCTTGCCAGGGCCGAGCGCCCGCCGCGCGCCCGCGCGCGCTTCCCGTCTTTCCCTTC 60
Db 55 ATGCGCGGCTCTGCTGCGCGCGCCCGCGCGCGCGCGCGCGCTTCCCGTCTTTCCCTTC 114
Qy 61 CCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 115 CC-----GCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 159
Qy 121 GTCCCGCGCTCAGTGCCAGAACCTCGCTGCGGATCTCCGAGGCTGACTCTATCTCACC 180
Db 160 GTCCCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 219
Qy 181 CGGTTTGAGCGGCTCTATACGTACAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Db 220 CGGTTTGAGCGGCTCTATACGTACAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 279
Qy 241 ACACCTTACGTCGCTGAGCGGATAGCATCTTCCGTTTAAACCTTCTCTCTCTCTCTCTCTCT 300
Db 280 ACACCTTATGTTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 339
Qy 301 AGACCCGAGGATCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 340 AGACCCGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 399
Qy 361 GGCAAGAAAGAGGACGAATGTACAAATTTTATCCAGATTTCTCGCCATTTGTCAATGCCTCT 420
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Db 400 GGCAAGAAAGAGGACGAATGTACAAATTTTCTCCAGATTTCTCGCCATTTGCCAATGCCTCT 459
Qy 421 CACCTCTCAGTCGCGCACCTTTCGCTTTTATCCGAGTCCGCGGTTTATGATGTGTCC 480
Db 460 CACCTCTCAGTCGCGCACCTTTCGCTTTTATCCGAGTCCGCGGTTTATGATGTGTCC 519
Qy 481 AGTTTCCAGCAGGTTGAAAGACTTGAGAGCGCGCGCGGGAATCTCCTTTTGGAGCCAGCT 540
Db 520 AGTTTCCAGCAGGTTGAAAGACTTGAGAGTGGCGCGCGGGAATCTCCTTTTGGAGCCAGCT 579
Qy 541 CAACGGTCAGCAGCTGTAATGGCTGGGGGCTCTCTACACCGCCACTGTGGAAGAACTTC 600
Db 580 CAGCGGTGAGCAGCTGTAATGGCTGGGGGCTCTCTATGTCGCACTGTGAAAACTAC 639
Qy 601 CTGGGAGCTGAGCCCATCATCTCCGAGCTGTGGTGGAGCTGAGGACTGGATTCGACACA 660
Db 640 CTGGGAGCTGAGCCCATCATCTACCAAGAACATGCGTGGCGAGGACTGGATTCGACACA 699
Qy 661 GAGACCTTGTCTATCTCTGCTTAAATGCTCCAGCCCTTTGTGCGAGCTATGGTCTTGAGCCCA 720
Db 700 GATACCTTGCCTTCTGCTGAGCGCCAGCCCTTTGTGCGAGCGCTTGCGCCTTGAGCCCA 759
Qy 721 GCTGAGTGGGGGATGAAGATG 742
Db 760 GCCGAATGGGGGATGAAGATG 781
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RESULT 5

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US-10-188-246-15
; Sequence 15, Application US/10188246
; Publication No. US20030087274A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.,
; APPLICANT: Boldog, Ferenc,
; APPLICANT: Casman, Stacie,
; APPLICANT: Edinger, Shlomit,
; APPLICANT: Gerlach, Valerie,
; APPLICANT: Gorman, Linda,
; APPLICANT: Li, Li,
; APPLICANT: Malyankar, Uriel,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Peyman, John,
; APPLICANT: Shenoy, Suresh,
; APPLICANT: Shimkets, Richard,
; APPLICANT: Vernet, Corine A. M.,
; APPLICANT: Voss, Edward
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND MET
; FILE REFERENCE: 21402-397B US
; CURRENT APPLICATION NUMBER: US/10/188,246
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 60/303046
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/304502
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/305011
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/306085
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 60/326981
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/360923
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/363636
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/373063
; PRIOR FILING DATE: 2002-04-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Custom
; SEQ ID NO 15
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Homo sapiens
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Qy	1142	TGCCCCAGCCACGCTGGAGGTGCATGCCCAACAACATGAAGCTCCAGCAGTTGGAT	1201
Db	1218	TACCCAGCCCTGGCCTGGCTCGTCGATTAAACAACATGGCATCGCGCCACGGCTACACCA	1277
Qy	1202	CCTCACTCTCCCTGCACAGCCGGTGTACCTTTTATCAGAGACCACTCTCTCATGGACA	1261
Db	1278	GCTCCCTGGAGCTTACCGGACAACATCCTAACTTCGTCAAGAAGCACCCGCTGATGGAGG	1337
Qy	1262	GGCCCGTGTTCCCGGCTGACGGCGGCCCTGCTGGTCACTACAGATACAGCCATATCTCA	1321
Db	1338	AGCAGGTGGGGCCCTCGGTGGAGCGGCCCTGCTGCTGTAAGAAGGGACCAACTTCACCC	1397
Qy	1322	GATCGTGGCCCCACAGGGTGACCAAGCTCTCAGGGAAAGAATATGAGTGCCTCTACCTGG	1381
Db	1398	ACCTGGTGGCGGACCGGTTACAGGACTTCATGGAGCCACCTATACAGTCTGTTCAATTG	1457
Qy	1382	GGACAGGAGTGGACACCTCCACCAGGCTGTGGGCATTTGGAGTCACTCAGTGTCTTTGG	1441
Db	1458	GCACAGGAGACGGCTGGCTGCTCAAGGCTGTGAGCCTGGGGCCCTGGGGTTCACCTGATTG	1517
Qy	1442	AGGATCTGGCCTTGTTT---CCCAGAACCCAGCCGGTTGAGAGCATGAATTTGATACCAG	1498
Db	1518	AGAGCTGCAGCTGTTTTCACAGGAGGCCCATGAGAAGCCCTGGTCTATCTCAGAGCAAGA	1577
Qy	1499	ATTGGGTCTCTGGTGGGCTCCCATACTGAGGTGACACAAGTGAACACCAGCAACTGTGGCC	1558
Db	1578	AGCTGCTCTTTGGCGCTCCCGTCTCAGCTGGTGCAGCTGCCCGTGGCCGACTGCATGA	1637
Qy	1559	GTCTCCAGAGCTCTCGGAGTGTATCTGTGCCCCAGGACCCCGTGTGGCCCTGGAGCTTCC	1618
Db	1638	AGTATCGCTCCTGTGCAGACTGTGTCTCTCGCCGGGACCCCTATTGGCCCTGGAGCGTCA	1697
Qy	1619	GGCTTGATGTTGTGGGCCCAACCGCGCA	1649
Db	1698	ACACGACCCGCTGTGTGGCCGTGGGTGGCCA	1728

RESULT 7

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RESOLUT 7
US-10-003-152-11
; Sequence 11, Application US/10003152
; Publication No. US20020151494A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meijia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: No. US20020151494A1e1 Amino Acid Sequences for Human Semaphorin-1
; FILE REFERENCE: 15966-554 Cura-54 CON-S12
; CURRENT APPLICATION NUMBER: US/10/003,152
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 2155
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (166)..(1935)
US-10-003-152-11

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Query Match	10.7%	Score 248.6;	DB 13;	Length 2155;
Best Local Similarity	52.1%	Pred. No. 8e-63;		
Matches 704;	Conservative	0;	Mismatches 629;	Indels 18; Gaps 6;
QY	308	GAAGGATCGACTGGTACCTGAGACTCACAGACAGAACTCGAGGAAGAAAGGCAAG-	366	

[illegible]

Db 1490 GCACAGAGAGCGCTGGCTGCTCAAGGCTGTGAGCCTGGGGCCCTGGGTTCACTGATG 1549
QY 1442 AGGATCTGGCTTGT---CCCAAGAACACAGCCGTTGAGAGCATGAAATTTGACACG 1498
Db 1550 AGGAGCTGACGCTGTTGACCAAGAGCCCATGAGAAGCCCTGGTGTCTATCTCAGAGCAAGA 1609
QY 1499 ATTGGCTCTGGTGGGCTCCCATCTAGAGGTGACAAAGTGAACACCAAGCAACTGTGGCC 1558
Db 1610 AGCTGCTCTTGGCCGCTCCCGCTCTCAGCTGGTGCAGCTGCCGCTGGCGGACTGCATAA 1669
QY 1559 GTCTCAGAGCTGCTGGAGTGTATCTGTGCCCCAGGACCCCGTGTGGGCTGAGGCTTCC 1618
Db 1670 AGTATCGCTCTGTGACAGTGTGTCTGTGCCGAGACCCCTATTGGCCTGAGCGTCA 1729
QY 1619 GGCTTGATGTTGTGGGCCACAGCCGGCGA 1649
Db 1730 ACACAGCCGCTGTGTGGCGTGGGTGGCCA 1760

RESULT 8
US-10-002-050-11
: Sequence 11, Application US/10002050
: Publication No. US20030032095A1
: GENERAL INFORMATION:
: APPLICANT: Shimkets, Richard
: APPLICANT: Fernandes, Elma
: APPLICANT: Vernet, Corine
: APPLICANT: Yang, Meijia
: APPLICANT: Boldog, Ferenc
: APPLICANT: Herrmann, John
: TITLE OF INVENTION: No. US20030032095A1el Nucleic Acid Sequences Encoding Human Semaph
: FILE REFERENCE: 15966-534 Cura-54 CON-S14
: CURRENT APPLICATION NUMBER: US/10/002,050
: CURRENT FILING DATE: 2001-11-02
: PRIOR APPLICATION NUMBER: 09/604,286
: PRIOR FILING DATE: 2000-06-22
: PRIOR APPLICATION NUMBER: 60/140,584
: PRIOR FILING DATE: 1999-06-23
: NUMBER OF SEQ ID NOS: 49
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 11
: LENGTH: 2155
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (166)..(1935)
US-10-002-050-11

Query Match 10.7%; Score 248.6; DB 14; Length 2155;
Best Local Similarity 52.1%; Pred. No. 8e-63;
Matches 704; Conservative 0; Mismatches 629; Indels 18; Gaps 6;

QY 308 GAAGGATGACGTGGATGTTACCTGAGACTCAGACAGAGACTGCAGGAAGAAGCAAG- 366
Db 419 GAGCGATCTCTGGGAGGCCCGCTGGAGAAGAGACTGAGTATCCAGAAGGGAAGA 478
QY 367 --AAAGAGGACGAATGTCAAAATTTATCCAGATTCCTGCCATTGTCAATGCTCTCAC 424
Db 479 ACAACAGACCGAGTCTTCACTTATCCGCTTCTGTGAGCCCTACAATGCTCCACC 538
QY 425 TCCTCAGCTGGCGACCTTCGCTTTTGTATCCGAAGTGGGGGTTAATGATGTCCAGTT 484
Db 539 TGTACGTCGTGTGACACTACGGCTTCCAGCCCAAGTGCACTAGCTCAACATGCTCACCT 598
QY 485 TCCA---GAGGTTGAAAGACTGTGAGAGCGCGCGGGGAAATGCTCTTTGAGCCAGCTC 541
Db 599 TCACCTTGGAGCTGAGAGTTTGAAGATGGGAAGGCAAGTGTCCCTATGACCCAGCTA 658
QY 542 AACGGTCAAGCAGCTGTAAATGGCTGGGGGGTCTCTTACACCCGCACTGTGAAGAAGCTCC 601
Db 659 AGGGCCATGCTGGCCTTCTGTGGATGGTGTACTGTACTGCGGCACACTCAACAAGCTTCC 718

QY 602 TGGGGACTGAGCCCATCATCTCCCGAGCTGTGGGTGAGCTGAGGACTGATTCGAACAG 661
Db 719 TGGGCACGAAACCCATTATCTTGCCTAACATGSSGC---CCCACCACTCCATGAAGACAG 775
QY 662 AGACCTTGTATCTCTGGCTTAATGCTCCAGCCCTTTTCCGAGCATATGCTCTGAGCCCA 721
Db 776 AGTACCTGGCCTTTTGGCTCAAGCAACCTCACTTTGTAGGCTCTGCTCATGTACCTGAGA 835
QY 722 CTGAGTGGGGGATGAAGATGGAGCAGTGAATCTTTTTTTTCTTCTCAGGAGACCTCC 781
Db 836 GTGTGGGAGCTTCACGGGGAGGACGACAAAGTCTACTTCTTCTCAGGAGCGGGCAG 895
QY 782 GAGTGTGGAGTCTTATGAGCGCATCAAGGTCCCAAGAGTGGGCCCGAGTGTGTGCGGG 841
Db 896 TGGAGTCCGACTGCTATGCGGAGCAGTGGTGGCTCGTGTGGCCGCTGTCTGCAAGGG 955
QY 842 ACCTTGGGGGAGGAAGACCTTTCAGCAGAGATGGAGAGGTTTCTTGAAGGCTGACCTGC 901
Db 956 ATATGGGGGGCGCACGACCCCTGCAGAGGAAGTGGACCACTTCTTGAAGGCGCGCTG 1015
QY 902 TGTGCCACGGGCCGAGCATGGCCGGCTCTCGGGGTCTGCAAGGCTATGGCAGAGCTTC 961
Db 1016 CATGCTCTGCCCGAAGTGGCAGCTTACTTCAACCAGCTGCAGGCGATG---CACACC 1072
QY 962 GGCCTCAGCCTGGAGCGGAACCCCATCTTTTATGGGATCTTTTCTCCAGTGGGAAG 1021
Db 1073 TGCAGGACACCTCTCTGGCACACACACCTCTTCTTGGGGTTTTCAGACACAGTGGGTG 1132
QY 1022 GAGCTGCCATCTCTGCTGTGTGCTTCCGACCCCAAGACATCCGGGCGAGTGTCAATG 1081
Db 1133 ACATGTACCTGTGGCCCATCTGTGAGTACCAGTGTGAAGAGATGCCAGCGGTGTTGAG 1192
QY 1082 GTCCCTTTTAGAGAGCTAAACATGACTGCAACAGGGGACTGCTGTCTATGGCAACAGG 1141
Db 1193 GCCCTATAAGAGTACCATGAGGAGCCAGAGTGGGACCGCTACACTGACCT--G 1249
QY 1142 TGCCCCAGCCAGACCTGAGAGTGCATCGCAACAACTGAGCTTCCAGAGTGTGGAT 1201
Db 1250 TACCCAGCCCTGGGCTGGCTGCTGATTAACAACTGGCATGGCCACCGCTACACCA 1309
QY 1202 CCTCACTCTCCCTGCCAGACCGCTGCTCACCTTTTATCAGAGACCACTCTCATGACA 1261
Db 1310 GCTCCCTGAGCTACCCGACAACTCTCAACTTCGTCAAGAGACCCCGCTGATGGAG 1369
QY 1262 GGCCTGCTTCCGCTGACGCGCCCTCTGCTGCTACTACAGATACAGCTATCTCA 1321
Db 1370 AGCAGTGGGGCTCGGTGGAGCCGCCCTGCTCTGAGAGGCGCACTTCACCC 1429
QY 1322 GAGTGTGGCCACAGGTTGACAGCTCTCAGGGAAGAAATATGACGTGCTCTACCTGG 1381
Db 1430 ACCTGTGGCCGACCGGTTACAGGACTTGTGAGGACCACTATACAGTGTCTCATTTG 1489
QY 1382 GCACAGAGATGGACACCTCCACCGGCTGTGCGCATTTGGAGCTCAGTGTCTTGG 1441
Db 1490 GCACAGGAGACGGCTGGCTGCTCAAGGCTGTGAGCCTGGGGCCCTGGGTTCACCTGAT 1549
QY 1442 AGGATCTGGCTTGT---CCCAAGAACACAGCCGTTGAGAGCATGAAATTTGACACG 1498
Db 1550 AGGAGCTGAGCTGTTTGAACAGGACCCATGAGAGCCTGGTGTATCTCAGAGCAAGA 1609
QY 1499 ATTGGCTCTGTGGGCTCCCATACTGAGGTGACACAAAGTGAACACCAAGCAACTGTGG 1558
Db 1610 AGCTGCTCTTTCGCGCTCCCGCTCTCAGCTGTGTGAGCTGCGCGTGGCCGAGTGCATAA 1669
QY 1559 GTCTCAGAGCTGCTGGAGTGTATCTTGGCCAGGACCCCGTGTGGCCTGGAGCTTCC 1618
Db 1670 AGTATCGCTCTGTGACAGACTGTCTCTCGCCCGGAGCCCTATTGCGCCTGGAGCGTCA 1729
QY 1619 GCTTGTGATGCTGTGTGGCCACAGCGCGCA 1649
Db 1730 ACACAGCCGCTGTGTGGCGTGGGTGGCCA 1760

RESULT 9

US-10-002-304-11
; Sequence 11, Application US/10002304
; Publication No. US20030036185A1
; GENERAL INFORMATION:
; APPLICANT: Shinkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meijia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: Polynucleotides and polypeptides encoded thereby
; FILE REFERENCE: 15966-554 Cura-54 CON-S8
; CURRENT APPLICATION NUMBER: US/10/002.304
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 2155
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (166)..(1935)
US-10-002-304-11

Query Match 10.7%; Score 248.6; DB 14; Length 2155;
Best Local Similarity 52.1%; Pred. No. 8e-63;
Matches 704; Conservative 0; Mismatches 629; Indels 18; Gaps 6;

QY	308	GAAGGATCGACTGATGTTACTGAGACTCACACAGAACTGACGAGGAAGAGCGAAG-	366
DB	419	GAGCGATCTCCTGGAGGCCCCCGTGGAGAAAGAACTGAGTGTATCCAGAAAGGA	478
QY	367	--AAAGAGAGCAATGTCACAAATTTATCCAGATTCTGCCATTGTCAATGCCCTCAC	424
DB	479	ACACAGACGAGTGTTCAACTTCATCCGCTTCTTGCAGCCCTACAAATGCCCTCCAC	538
QY	425	TCCTCAGCTGGGACCTCTTTCGTTTATCCGAAGTGGGGGTTATTGATGTCTCAAGTT	484
DB	539	TGTACGCTGTGGCACCCTACGCCCTTCCAGCCAAAGTGCACCTAGCTCAACATGCTCACT	598
QY	485	TCCA--GCAGTTGAAGACTTGAGAGCGCGCGGGGAATGTCTTTTTCAGCCAGCTC	541
DB	599	TCACCTTGGAGCATGGAGAGTTTGAAGATGGGAAGGGCAAGTGTCCCTATGACCCAGCTA	658
QY	542	AACGCTCAGCAGCTGTAATGGCTGGGGCGTCTCTACACCGCCACTGTGAAGAACTTCC	601
DB	659	AGGCCATGCTGGCCTTCTTGTGGATGTTGAGCTGTAATCGGCCACACTCAACACTTCC	718
QY	602	TGGGACTGAGCCCATCATCTCCGAGCTGTGGTTCGAGTGCAGAGTGGATTTCGAACAG	661
DB	719	TGGCAGCAAGAACCATTAATCTCGGTAACTATGAGGCTTCCAGCTCCATGAAGACAG	775
QY	662	AGACCTTGTATCTCTGGCTTAATGCTCCAGCTTGTGCGAGCTATGCTCTGAGCCAG	721
DB	776	AGTACCTGGCCTTTGGGCTCAACGAACCTACTTGTAGGCTCTGCCCTATCTACCTGAGA	835
QY	722	CTGAGTGGGGGATGAAGATGAGACGATGAAATCTTTTTCCTACGGAGACCTGCC	781
DB	836	GTGTGGGAGCTTCACGGGGACGACGACAGGCTACTTCTTCTCAGGAGCGGGCAG	895
QY	782	GAGTGTGGACTCTTATGAGCGCATCAAGGTCCCAAGAGTGGCCGAGTGTGTGGGGGG	841
DB	896	TGGAGTCCGACTGCTATCCGAGCAGAGTGGTGGCTCGTGTGGCCGCTGCTCAAGGCG	955
QY	842	ACCTTGGGGGAGGAGACCTTTCAGCAGAGATGGACGACCTTCTGAAGCTGACCTGC	901
DB	956	ATATGGGGGGCGACGGACCTTGCAGAGGAAGTGGACCACTTCTTCTGAAGCGCGGTG	1015

QY	902	TGTGCCAGGCGCCGAGCATGGCCGGGCTCCGGGGTTCTGAGGCTATGACAGGCTTC	961
DB	1016	CATGCTCTGCCCGCAACTGGCAGCTCTACTTCAACCAAGCTCAGCGGATG--CACACCC	1072
QY	962	GGCTCAGCCTGGAGCGGGAACCCCCATCTTTTATGGGATCTTTTCTCCAGTGGGAAG	1021
DB	1073	TGCAGGACACCTCCTGGCACAACACACCTCTTTTGGGGTTTTCAGACAGTGGGTG	1132
QY	1022	GAGTGGCATCTCTGCTGTGCTTCCGACCCCAAGACATCGGSCAGCTGCTGAATG	1081
DB	1133	ACATGTACTCTCGGCCATCTGTGAGTACCACTTGGGAAGATCCAGGGGTGTTTGAGG	1192
QY	1082	GTCCCTTTAGAGAGCTAAACATGACTGCAACAGGGGACTCCCTGTCTATGGACAACGAG	1141
DB	1193	GCCCTATATAGGAGTACCATGAGGAAGCCCAAGAGTGGACCGCTACACTGACCT--G	1249
QY	1142	TGCCCCAGCCAGACCTGGAGAGTGCATCGCCACAACATGAAGTCCAGCAGTTTGAT	1201
DB	1250	TACCCAGCCCTCGGCTGCTGTCATTAACAACATGGCATCGGCGCCACCGCTACACCA	1309
QY	1202	CCTCACTCTCCCTGCCAGACCGCTGCTCACTTTATCAGAGACCACTCTCATGGACA	1261
DB	1310	GCTCCCTGGAGCTACCGGACAACATCTCACTTCGTCGAAGAGCACCCGCTGATGGAG	1369
QY	1262	GGCCGCTGTTCCCGCTGACGGCGCCCTGCTGCTGCTCACTACAGATACAGCCTATCTCA	1321
DB	1370	AGCAGGTGGGCTCGGTGGAGCGCCCTGCTGCTGGAAGAGGCAACCACTTCACCC	1429
QY	1322	GAGTGTGGCCACAGGCTGACACGCTCTCAGGAAAGATATGACGTGCTTACCTGG	1381
DB	1430	ACCTGGTGGCGACCGGCTTACAGACTTGTATGGAGCCACCTATACAGTGTCTCATTTG	1489
QY	1382	GGACAGAGGATGGACACCTCCACCGGCTGCGCATTTGGAGCTCAGCTCAGTGTCTGG	1441
DB	1490	GCACAGGAGAGGCTGCTCAAGGCTGTGAGCTGGGGCCTGCGGCTTCACTGATTG	1549
QY	1442	AGGATCTGGCCTTGT---CCAGAACACACAGCCGCTTGAGAGCATGAAATGTACCAACG	1498
DB	1550	AGGAGCTGCAGCTGTTTGACCAAGAGCCCATGAGAAGCTTGTCTATCAGAGCAAGA	1609
QY	1499	ATTGGCTCTGGTGGCTCCCATCTAGGTGACACAGTGAACACCAAGCACTGTGGCC	1558
DB	1610	AGCTGCTTTTGGCGGCTCCCGCTCTCAGCTGCTGACGCTGCCGCTGGCCGACTGCATAA	1669
QY	1559	GTCCTCAGAGCTGCTCGGAGTGTATCTCGGCCAGGACCCGCTGTGCCCTGGAGCTTCC	1618
DB	1670	AGTATCGCTCTGTGCAGACTGTCTCTCGCCCGGACCCCTATTTGCCCTTGGAGCGTCA	1729
QY	1619	GGCTTGATGCTTGTGGCCCAAGCCGCGCA	1649
DB	1730	ACACAGCGCTGTGTGCGCGCTGGGTGSCCA	1760

RESULT 10

US-10-003-152-21
; Sequence 21, Application US/10003152
; Publication No. US20020151494A1
; GENERAL INFORMATION:
; APPLICANT: Shinkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meijia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: No. US20020151494A1el Amino Acid Sequences for Human Semaphorin
; FILE REFERENCE: 15966-554 Cura-54 CON-S12
; CURRENT APPLICATION NUMBER: US/10/003.152
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23

; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 2156
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (166)..(2037)
; NAME/KEY: variation
; LOCATION: (1)..(2156)
; OTHER INFORMATION: N may be any nucleotide
US-10-003-152-21

Query Match 10.7%; Score 248.6; DB 13; Length 2156;
Best Local Similarity 52.1%; Pred. No. 8e-63;
Matches 704; Conservative 0; Mismatches 629; Indels 18; Gaps 6;

QY	308	GAAGGATCGACTGGATGTAACCTTATCCAGATTTCTGCCAATTTGTCATGTCCTCACC	366
DB	419	GAGCGATCTCCTGGGAGGCCCGGTGGAGAAAGACTGAGTGTATCCAGAAAGGAAGA	478
QY	367	--AAGAGACCAATGTCACAAATTTATCCAGATTTCTGCCAATTTGTCATGTCCTCACC	424
DB	479	ACAACAGACCCAGTGTCTCAACTTCACCGCTTCTCGAGCCCTACAAATGCTCCCAAC	538
QY	425	TCCTCAGCTGCGGCACCTTCGCTTTTGATCCGAAGTGGGGTATTGATGTGTCAGTT	484
DB	539	TGTACGTCTGTGGCACCCTAGCGCTTCCAGCCCAAGTGACCTTACGTCAACATGCTCACT	598
QY	485	TTCCA--GCAGTTTGAAGACTTTGAGAGGGCGGGGAAATGTCTTTTGGAGCGCTC	541
DB	599	TCACCTTGGAGCATGGAGATTGAAGATGGGAAGGCAAGTGTCCCTATGACCCAGCTA	658
QY	542	RACGCTCAGCAGCTTAATGGCTGGGGCTCTTACACCCGCACTGTGAAGAACTTCC	601
DB	659	AGGGCCATCTGGCCCTCTTGTGGATGGTGAGCTGTACTCGGCCACACTCAACAACCTCC	718
QY	602	TGGGACTGAGCCCATCATCTCCGAGTGTGGGTGAGCTGAGGACTGGATTTCGAACAG	661
DB	719	TGGGACGGAACCCATATCTCGCTGAACATGGGC---CCACCACTCCATGAAGACAG	775
QY	662	AGACCTTGTCATCTCGGCTTAATGCTCCAGCCTTGTGCGCAGCTATGTCCTGAGCCGAG	721
DB	776	AGTACTCGCCCTTTTGGCTCAACGAACCTCACTTTGTAGGCTCTGCTATGTACCTGAGA	835
QY	722	CTGAGTGGGGGATGAAGATGAGAGATGAATCTTTTCTTCTCAGGAGACCTCCC	781
DB	836	GTGTGGCGAGCTTACGGGGGACGACGACAAAGGTCTACTTCTTCTCAGGGAGCGGGCAG	895
QY	782	GAGTGTGACCTCTATGAGCGCATCAAGTCCCAAGAGTGGCCGAGTGTGTGGGGGG	841
DB	896	TGGAGTCCGACTGCTATGCCGAGAGGTGGTGGCTGTGTGGCCGCTGTCTCAAGGGCG	955
QY	842	ACCTTGGGGGAGGAAGACCTTTCAGCAGAGATGAGCAGCTTTCTGAAGGCTGACCTGC	901
DB	956	ATATGGGGGGCGACGGACCTCTGCAGAGGAAGTGGACCACTTCTCTGAAGGCGGCGCTGG	1015
QY	902	TGTGCCAGGGGCCGAGCATGCGCGGCTCCGGGTTCTCGAGGCTATGGCAGAGCTTC	961
DB	1016	CATGCTCTGCCCGCACTGGCAGCTCTACTTCAACAGCTGCAGCGCGATG---CACACC	1072
QY	962	GGCCTCAGCCTGGAGGGGAACCCCATCTTTTATGGATCTTTTCTCCCTCCAGTGGGAAG	1021
DB	1073	TGCAGGACACCTCTCTGGCAGACACACCACTTCTTTGGGTGTTTCAAGCAGACTGGGTG	1132
QY	1022	GAGCTGCCATCTCTGCTGTGTGCTTCCGACCCCAAGACATCCGGGCGAGTGTGAATG	1081
DB	1133	ACATGTACCTGTGCGCCATCTCTGTAGTACCACTTGGAAAGAGATCCAGCGGGTGTGTTGAG	1192
QY	1082	GTCCCTTTAGAGACTAAACATGACTGCAACAGGGGACTGCTGTCTATGGAACAGAGG	1141
DB	1193	GCCCTATAAGGATGACCATGAGGAAGCCAGAAAGTGGGACCGCTACACTGACCT---G	1249

RESULT 11
US-10-002-050-21
; Sequence 21, Application US/10002050
; Publication No. US2003032095A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meijia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: No. US20030032095A1el Nucleic Acid Sequences Encoding Human Se
; FILE REFERENCE: 15966-554 Cura-54 CON-S14
; CURRENT APPLICATION NUMBER: US/10/002,050
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 2156
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (166)..(2037)
; NAME/KEY: variation
; LOCATION: (1)..(2156)
; OTHER INFORMATION: N may be any nucleotide
US-10-002-050-21

Query Match 10.7%; Score 248.6; DB 14; Length 2156;
Best Local Similarity 52.1%; Pred. No. 8e-63;

Matches 704; Conservative 0; Mismatches 629; Indels 18; Gaps 6;			
Qy	308	GAAGGATCGACTGGTACCTGAGACTCACACAGAACTGCAGGAAGAAAGGCAAG- 366	
Db	419	GAGGATCTCTGGAGGCCCCCGTGGAGAAGACTGAGTGTATCCAGAAAGGGAAGA 478	
Qy	367	--AAAGAGGAGAAATGCAAAATTTATCCAGATTCGCGCAATGTCAAATGCCCTCAC 424	
Db	479	ACAAACAGACGAGTGTCTAACTTCATCGCTTCCTCGAGCCCTACAATGCCCTCCACC 538	
Qy	425	TCCTCAGCTGGGACCTTCGCTTTTATCCGAAGTGGGGTTATGATGTGTCAGTT 484	
Db	539	TGTACGTCTGTGGCACCCTACGCTTCAGGCCCCAAGTGCACCTACGTCACCT 598	
Qy	485	TCCA--GCAGGTTGAAGACTTCGAGAGCGCCCGGGGAAATGTCCTTTTGGAGCAGCTC 541	
Db	599	TCACCTTGGAGCATGGAGAGTTTGAAGATGGGAAGGCAAGTGTCCCTATGACCCAGTA 658	
Qy	542	AACGGTCAGCAGCTGTAATGGCTGGGGGGTCTCTACACGGCCACCTGTGAAGAACTTCC 601	
Db	659	AGGCCCATGCTGGCTCTCTTGTGATGGTGAAGCTGTACTGGGCCACACTCAACAACCTCC 718	
Qy	602	TGGGAGCTAGCCCATCATCTCCGAGCTGTGGGTCGAGCTGAGGACTGGATTGCAACAG 661	
Db	719	TGGCAGCGAACCCTATCTCGCTAACATGAGGCG--CCACCACTCCATGAAGACAG 775	
Qy	662	AGACCTTGTCTATCTCGCTTAATGCTCCAGCCTTTGTCGAGCTATGCTCTGAGCCAG 721	
Db	776	AGTACCTGGCTTTTGGCTCAACGAACCTCACCTTGTAGGCTCTGCCTATGACTCTGAGA 835	
Qy	722	CTGAGTGGGGGATGAAGATGGAGACGATGAATCTTTTTTTTCTTCAACGAGACCTTCC 781	
Db	836	GTGTGGGAGCTTTCACGGGGGACGACGACAAAGTCTACTTCTTCAAGGAGCGGGCAG 895	
Qy	782	GAGTGTGGACTCTATGAGGCGATCAAGTCCCAAGAGTGGCCCGAGTGTGCGGGG 841	
Db	896	TGGAGTCGAGCTATGTCGAGAGAGTGTGGCTGTGGTGGCCCGTCTGCAAGGCG 955	
Qy	842	ACCTTGGGGGAGAAACCCCTTCAGCAGAGATGAGCAGCCTTTCTGAAGCTGACCTGC 901	
Db	956	ATATGGGGGGCGACGACCCCTGCAGAGGAAGTGGACCACGCTTCTGAAGCGCGCTGG 1015	
Qy	902	TGTCGCCAGGCGCCGAGTGGCGGGCTCCGGGGTTCGACGGCTATGACAGAGTTC 961	
Db	1016	CATGCTGTGCCCCAACTGGCAGCTCTACTTCAACCACTGACAGCGCATG---CACACC 1072	
Qy	962	GGCTCTAGCTGGAGCGGAACCCCATCTTTTATGGATCTTTTCTCCAGTGGGAAG 1021	
Db	1073	TGCAGGACACCTCTCGCACACACACACCTTCTTTGGGTATTTCAAGCAGTGGGGTG 1132	
Qy	1022	GAGTGGCATCTCTGCTGTGTGCTTCCGACCCCAAGACATCCGGGCGAGTGTGAATG 1081	
Db	1133	ACATGTACCTGTGCGCATCTGTGAGTACCAGTTTGAAGAGATCCAGCGGTGTTGAGG 1192	
Qy	1082	GTCCCTTAGAGACTAAACATGATGCAACAGGGGACTGCTGTATGAGCAACAGG 1141	
Db	1193	GCCCTATAAGAGATACCATGAGGAAGCCCAAGAGTGGGACCGGTACACTGACCTC---G 1249	
Qy	1142	TGCCCCAGCCCGAGACCTGGAGAGTGCATCGCCCAACATGAAGCTCCAGCAGTTGGAT 1201	
Db	1250	TACCCAGCCCTCGGCTGTGCTGTGATTAACAACCTGGCATCGGCGCCACGGGTACACCA 1309	
Qy	1202	CCTCAGCTCTCCCTGCCAGACCGCTGTCTACCTTTATCAGAGCACCCCTCTCATGGACA 1261	
Db	1310	GCTCCCTGGAGCTACCCGACAACATCTCACTTCGTCAAGAACACCCGCTGATGGAGG 1369	
Qy	1262	GGCCCGTGTCCCGGCTGACGGCGCCCGCTGTGCTGCTACATACAGATACAGCCTATCTCA 1321	
Db	1370	AGCAGGTGGGGCTTCGGTGGAGCGCCCGCTGCTCGTGAAGAAAGGCAACAACTTCACCC 1429	
Qy	1322	GAGTGTGGCCACAGGCTGACCACTCTCAGGGAAGAAATATACGCTGCTCTACCTGG 1381	
Db	1430	ACCTGGTGGCGGACCGGTTACAGGACTTGTATGAGCCACCTATACAGTGTCTTCATTG 1489	

Qy	1382	GGACAGGATGGACACCTCCACCGGCTGTGCGCATTTGGAGCTCAGCTCAGTCTCTTG 1441	
Db	1490	GCACAGGAGCGGTGCTCAAGGCTGTGACGCTGGGCGCTTGGTTCCACCTGATTG 1549	
Qy	1442	AGGATCTGGCCTTTT---CCAGAACACACAGCGGTTGAGAGCATGAATTTGACCAAG 1498	
Db	1550	AGGAGCTGCAGCTCTTTTGACGAGGAGCCCATGAGAAGCCTGTGTCTATCTCAGAGCAAA 1609	
Qy	1499	ATTGCGCTCGTGGTCCCATACTGAGGTGACACAAAGTGAACACCAAGCAACTGTGGCC 1558	
Db	1610	AGCTGCTCTTTGCGCGGTCCCGCTCTCAGCTGTGTCAGCTGCCGTGGCCGACTGCATTA 1669	
Qy	1559	GTCTCCAGAGCTGCTGGAGTGTATCTGCGCCAGGACCCCGTGTGCGCTTGGAGCTTCC 1618	
Db	1670	AGTATCGCTCTGTGACAGCTGTGTCTCGCCCGGACCCCTATTGCGCCTGGAGCGTCA 1729	
Qy	1619	GGCTGTGATGCTTGTGTGGCCACCGCCGCGA 1649	
Db	1730	ACACAGCGCTGTGTGGCGGTGGTGCCA 1760	

RESULT 12

US-10-002-304-21
; Sequence 21, Application US/10002304
; Publication No. US20030036185A1
; GENERAL INFORMATION:
; APPLICANT: Shlmkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meijia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herimann, John
; TITLE OF INVENTION: Polynucleotides and polypeptides encoded thereby
; FILE REFERENCE: 15966-554 Cura-54 CON-S8
; CURRENT APPLICATION NUMBER: US/10/002.304
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 2156
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (166)..(2037)
; NAME/KEY: variation
; LOCATION: (1)..(2156)
; OTHER INFORMATION: N may be any nucleotide
US-10-002-304-21

Query Match 10.7%; Score 248.6; DB 14; Length 2156; Best Local Similarity 52.1%; Pred. NO. 8e-63; Matches 704; Conservative 0; Mismatches 629; Indels 18; Gaps 6;			
Qy	308	GAAGGATCGACTGGTACCTGAGACTCACACAGAACTGCAGGAAGAAAGGCAAG- 366	
Db	419	GAGGATCTCTGGAGGCCCCCGTGGAGAAGAAAGACTGAGTGTATCCAGAAAGGGAAGA 478	
Qy	367	--AAAGAGGAGAAATGTCACAAATTTATCCAGATTCGCGCAATTTGTCATTCCTCACC 424	
Db	479	ACAACAGACGAGTGTCTCAACTTCATCCGCTTCTCGACGCCCTACAAATGCCCTCCACC 538	
Qy	425	TCCTCAGCTGGGCACTTTCGCTTTTGTATCCGAAGTGGGGTTTATGATGTGTCCAGTT 484	
Db	539	TGTACGTGTGGCACCTTACGCTTCCAGCCCAAGTGCACCTACGTCAACATGCTCACT 598	
Qy	485	TCCA---GCAGGTTGAAGAGCTTGAAGCGCGCGGGGAAATGCTCTTTTGGAGCGAGTC 541	

Db 599 TCACCTTTGAGCATGGAGAGTTTGAAGATGGGAAGGCAAGTGTCTCCCTATGACCCAGCTA 658
QY 542 AACGGTCAGACAGCTTAATGGCTGGGGCGTCTCTACACGCCCACTGTGAAGAAGTCTCC 601
Db 659 AGGGCCATGCTGGCCCTTCTTGTGGATGTTGAGCTGTACTCGGCCACACTCAACAAGTCTCC 718
QY 602 TGGGAGCTGAGCCCATCATCTCCCGAGCTGTGGTTCGAGCTGAGGAGTGGATTCTGAACAG 661
Db 719 TGGGCACGGAACCCATTAATCTCGCTTAACATGGGC---CCACCACTCCATGAAGACAG 775
QY 662 AGACCTTGTATCTCTGGCTTAATGCTCCAGCCTTTGTTCGACAGCTATGTTCTGACCCAG 721
Db 776 AGTACTCGCCCTTTTGGCTCAACGAACCTCACTTTGTAGGCTCTGCCTATGTACCTGAGA 835
QY 722 CTGAGTGGGGGATGAAGATGGAGAGATGAATCTTTTCTTCAAGGAGACCTCC 781
Db 836 GTGTGGGAGCTTACGGGGAGCAGACAGAGTCTACTCTTCTTCAAGGAGCGGGCAG 895
QY 782 GAGTGTGAGCTCTATGAGCGCATCAAGGTCCCAAGAGTGGCCGAGTGTGTGGGGG 841
Db 896 TGGAGTCCGACTGCTATCCGAGCAGGTGGTGGCTCGTGTGGCCGCTGTCTCAAGGGCG 955
QY 842 ACCTTGGGGAGGAGACCTTTCAGACAGATGACGACAGTCTTCTGAAGCTGACCTGCG 901
Db 956 ATATGGGGGGCAGCGGACCTTGCAGAGGAAGTGGACCACTTCTGAAGCGCGCGCTGG 1015
QY 902 TGTGCCCGAGGCGCAGCATGGCGGGCTCCGGGGTCTGCGAGCTATGGCAGAGCTTC 961
Db 1016 CATGCTCTGCCCGAAGTGGCAGCTCTACTTCAACCAAGCTGCAGCGGATG---CACACC 1072
QY 962 GGCCTCAGCTGGAGCGGGAACCCCATCTTTATGGATCTTTTCTCCAGTGGGAG 1021
Db 1073 TGCAGGACACCTCTCTGGCACAACACCACTTCTTTGGGGTTTTTCAAGCAGAGTGGGGTG 1132
QY 1022 GAGCTGCCATCTCTGCTGTGTGCTTCCGACCCCAAGACATCGGGCAGTGTGTAATG 1081
Db 1133 AGATCTACTCTGCGGCCATCTGTGAGTACCAAGTTGGNAGAGATCAGCGGGTGTGTGAGG 1192
QY 1082 GTCCCTTTAGAGAGTAAACATGACTGCAACAGGGGACTGCTGTATGACACACGAGG 1141
Db 1193 GCCCTATAGAGGTACCATGAGGAGCCCAAGAGTGGGACCGCTACACTGACCT---G 1249
QY 1142 TGCCTCAGCCAGACCTGGAGAGTGCATCGCCCAACACATGAAGTCCAGCAGTTTGAT 1201
Db 1250 TACCCAGCCCTCGGCTGCTGCTGATTAACAACTGGCATCGGGCCACGCTACACCA 1309
QY 1202 CACTACTCTCCTCGCAGCCGCTGCTCACTTTATCAGAGACCACTCTCATGGACA 1261
Db 1310 GCTCCTGGAGTACCCGACACATCTCTCAACTTCGTCAAGAAGCACCCTGTATGGAGG 1369
QY 1262 GCGCGCTGTCCGCTGACGGCCGCCCTGCTGCTCACTACAGATACAGCCTATCTCA 1321
Db 1370 AGCAGTGGGCTCGGTGGAGCCGCCCTGCTGCTGAAGNAGGCACTTCACTCC 1429
QY 1322 GAGTCGTGGCCACAGGTGACACGCTCTCAGGGAAGAATATGACGTGCTCTACCTGG 1381
Db 1430 ACTGCTGGCCGACCGGTTACAGGACTTGATGGAGCCACCTATACAGTGTCTTCAATTG 1489
QY 1382 GGACAGAGATGGACACCTCCACCGGCTGTGCGCATTTGGAGCTCAGCTCAGTGTCTGG 1441
Db 1490 GCACAGGAGAGCGGTGGCTGCTCAAGGCTGTGAGCCTGGGGCTTCACTGTATG 1549
QY 1442 AGGATCTGGCCTTGT---CCAGAACACACCGCTTGGAGAGCATGAATTTGACACG 1498
Db 1550 AGGAGCTGAGCTGTTTGACCCAGGAGCCCATGAGAAGCCTGCTGTATCTCAGAGCAAA 1609
QY 1499 ATTGGCTCGTGGGGTCCCATACTGAGGTGACACAAGTGAACACCAAGCACTGTGGCC 1558
Db 1610 AGCTGCTCTTGGCCGCTCCCGCTCTCAGCTGGTGCAGCTGCGCCGTGGCCGACTCATTA 1669
QY 1559 GTCTCCAGAGTGTCTGAGTGTATCTTGGCCGAGGACCCGCTGTGCGCCTGGAGCTTCC 1618
Db 1670 AGTATCGCTCTCTGTCAGACTGTCTCTCGCCCGGAGCCCTTATTGCGCCCTGGAGCGTCA 1729

QY 1619 GCGTTGATGCTTGTGTGGCCCAACCGCGCA 1649
Db 1730 ACACCAGCGCTGTGTGGCGTGGGTGCCA 1760

RESULT 13

US-10-003-152-13

; Sequence 13, Application US/10003152

; Publication No. US20020151494A1

; GENERAL INFORMATION:

; APPLICANT: Shimkets, Richard

; APPLICANT: Fernandes, Elma

; APPLICANT: Vernet, Corine

; APPLICANT: Yang, Melija

; APPLICANT: Boldog, Ferenc

; APPLICANT: Herrmann, John

; TITLE OF INVENTION: No. US20020151494A1el Amino Acid Sequences for Human Semaphori

; FILE REFERENCE: 15966-554 Cura-54 CON-S12

; CURRENT APPLICATION NUMBER: US/10/003.152

; CURRENT FILING DATE: 2001-11-02

; PRIOR APPLICATION NUMBER: 09/604, 286

; PRIOR FILING DATE: 2000-06-22

; PRIOR APPLICATION NUMBER: 60/140, 584

; PRIOR FILING DATE: 1999-06-23

; NUMBER OF SEQ ID NOS: 49

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 13

; LENGTH: 2284

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (166)..(1953)

; NAME/KEY: Variation

; LOCATION: (1)..(2284)

; OTHER INFORMATION: N may be any nucleotide

US-10-003-152-13

Query Match 10.7%; Score 248.6; DB 13; Length 2284;
Best Local Similarity 52.1%; Pred. No. 8.2e-63;
Matches 704; Conservative 0; Mismatches 62; Indels 18; Gaps 6;

QY 308 GAAGGATCGACTGGATGTTACCTGAGACTCAGACAGAACTGCAGGAAGAAAGCAAG- 366
Db 419 GAGGATCTCTGGGAGGCCCGCTGGAGAAAGAACTGAGTGTATCCAGAAAGGAAGA 478
QY 367 --AAGAGGAGATGTCAAAATTTTATCCAGATTCTCGCCATTTGCAATGCTCCTCACC 424
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QY 425 TCCTCAGCTGGGCACTTCGCTTTTGTATCGAAGTGGGGTTATGATGTGTCCAGTT 484
Db 539 TGTAGCTGTGGCACTTACGCTTCCAGCCCAAGTGCACCTACCTCAACATGCTCACT 598
QY 485 TCCA---CGAGTTGAAGACTTGAGAGCGCCGGGAAATGTCCTTTTGAAGCAGCTC 541
Db 599 TCACCTTGGAGCATGGAGATTTGAAGATGGAGGCAAGTGTCCCTATGACCCAGCTA 658
QY 542 AACGTCAGCAGCTGTATGCTGGGGCGTCTCTACACGCCCACTGTGAGAACTTCC 601
Db 659 AGGGCCATGCTGGCCCTTCTTGTGATGTTGAGCTGTACTCGGCCCACTCAACAACCTTC 718
QY 602 TGGGAGCTGAGCCCATCATCTCCCGAGCTGTGGGTCGAGCTGAGACTGGATTTCGAACAG 661
Db 719 TGGGCACGGAACCCATTAATCTCGCTAACATGGGCG---CCACCACTCCATGAAGACAG 775
QY 662 AGACCTTGTATCTCTGGCTTAATGCTCCAGCCTTTGTTCGACAGTATGTTCTGAGCCAG 721
Db 776 AGTACCTGGCCTTTTGGCTCAACGAACCTCACTTTGTAGGCTCTGCCTATGTACCTGAGA 835
QY 722 CTGAGTGGGGGATGAAGATGGAGAGCATGAATCTTTTCTTCTACGGAGACCTCCC 781

Db 836 GTGTGGGAGCTTCACGGGGACGACGACAGGCTTACTTCTTCCAGGAGCGGCAG 895
Qy 782 GAGTGTGGACTCTATGAGCGCATCAAGGTCCCAAGAGTGGCCCGAGTGTGTGCGGGG 841
Db 896 TGGAGTCCGACTGCTATGCGGAGCAGGTGTGGCTGTGTGGCCCGTGTGCAAGGCG 955
Qy 842 ACCTTGGGGGAGAAACCTTTCAGCAGAGATGAGCAGCTTTCCTGAAGGCTGACCTGC 901
Db 956 ATATGGGGGGCGACGACCTGCGAGAGAGTGGACCACTTCTGAAGGCGGGCTGG 1015
Qy 902 TGTGCCAGGCGCGAGCATGGCGGCGCTCCGGGTTCTGCAAGGCTATGGCAGAGTTC 961
Db 1016 CATGCTGTGCCGAACTGGCAGCTCTACTTCAACAGCTGGAGCGCAT---CACACC 1072
Qy 962 GGCTCAGCTGGAGCGGGAACCCCATCTTTTATGGATCTTTTCTCCAGTGGGAAG 1021
Db 1073 TGCAGGACACTCTCTGSCACAACACCACTTCTTTGGGTTTTCAGACGACTGGGGTG 1132
Qy 1022 GAGTGGCCATCTCTGTGTGTGTGCTTCCGACCCCAAGACATCCGGGCGAGTGTGAATG 1081
Db 1133 ACATGTACCTGTGCGGCATCTGTGAGTACCAGTTTGAAGAGATCCAGCGGGTGTTCAGG 1192
Qy 1082 GTCCCTTTAGAGAGTAAACATGACTGCAACAGGGGACTGCCTGTCTATGCACACAGG 1141
Db 1193 GCCCTATAGGAGTACCATGAGAGACCCAGAGTGGGACCGTACACTGACCT---G 1249
Qy 1142 TGCCCCAGCCGACCTGGAGAGTGCATCGCCCAACACATGAAGCTCCAGCAGTTTGGAT 1201
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Qy 1202 CTTCACTCTCCCTGCCAGAGCGGTGCTCACTTTATCAGAGACCACTTCTCATGAGCA 1261
Db 1310 GCTCCCTGGAGTACCCGCAACATCTCACTTCTGAAGAGCAACCCGCTGATGGAG 1369
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RESULT 14

US-10-002-050-13

; Sequence 13, Application US/10002050

; Publication No. US20030032095A1

; GENERAL INFORMATION:

; APPLICANT: Shimkets, Richard

; APPLICANT: Fernandes, Elma

; APPLICANT: Vernet, Corine

; APPLICANT: Yang, Meijia

; APPLICANT: Boldog, Ferenc

; APPLICANT: Herimann, John
; TITLE OF INVENTION: No. US20030032095A1el Nucleic Acid Sequences Encoding Human Se
; FILE REFERENCE: 15966-554 Cura-54 CON-S14
; CURRENT APPLICATION NUMBER: US/10/002,050
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 2284
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (166)..(1953)
; NAME/KEY: variation
; LOCATION: (1)..(2284)
; OTHER INFORMATION: N may be any nucleotide
US-10-002-050-13

Query Match

10.7%; Score 248.6; DB 14; Length 2284;
Best Local Similarity 52.1%; Pred. No. 8.2e-63;
Matches 704; Conservative 0; Mismatches 629; Indels 18; Gaps 6;

Qy 308 GAAGGATCGACTGGATGGTACCTGAGACTCACACAGAACTGCAGGAAGAAAGCGAAG- 366
Db 419 GAGCGATCTCTGGGAGGCCCCCGTGGAGAAAGAACTGATGTATCAGAAAGGGAAGA 478
Qy 367 --AAAGAGGACGAATGTCACAAATTTATCCAGATTCCTCGCATTTGTCAATGCCCTCTCAC 424
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Db 539 TGTACGCTCTGTGGCACCCTAGCCCTTCCAGGCCCAAGTGCACCTAGTCAACATGCTCACCT 598
Qy 485 TCCA---GCAGTTGAAGACTTCAGAGCGCGCGGGGAAATGTCCTTTTTCAGCCAGCTC 541
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Db 659 AGGCCATGTCTGGCTTCTTGTGATGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 718
Qy 602 TGGGAGTGAAGCCATCATCTCCGAGCTGTGGGTGAGCTGAGGACTGGATTGCAACAG 661
Db 719 TGGGACGGAACCCATTTATCTGCGTAAACATGGGGC---CCCACCACTCCATGAAGACAG 775
Qy 662 AGACCTGTCTATCTGCTTAATGCTCCAGCTTGTGTCAGCTATGCTGTCGAGCCAG 721
Db 776 AGTACCTGGCTTTTGGCTCAAGAACTTCACTTTTGTAGGCTTGCCTATGATACCTGAGA 835
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Qy 782 GAGTGTGGACTCTCTATGAGCGCATCAAGTTCACAGAGTGGGCCGAGTGTGTGCGGGGG 841
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Qy 842 ACCTTGGGGCAGGAAGACCTTTCAGCAGAGATGGAGAGCTTTCGAAAGGCTGACCTGC 901
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Job time : 522.387 secs

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GenCore version 5.1.6
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OW nucleic - nucleic search, using sw model

Run on: September 25, 2003, 17:51:04 ; Search time 571.81 Seconds
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2331	100.0	2331	19 AAV07280	Rat semaphorin W e
2	2331	100.0	4008	19 AAV07279	Rat semaphorin W e
3	2138.8	91.8	4024	21 AA287977	Mouse semaphorin W
4	1827.6	78.4	2971	22 AAF93776	Human cDNA encodin
5	1626	69.8	2893	20 AAX86126	DNA encoding SBSEM
6	1626	69.8	2894	20 AAX86127	EST sequence for D
7	1393.2	59.8	2315	19 AAV07281	Human semaphorin W
8	1391.2	59.7	1761	19 AAV07282	Human semaphorin W

9	654	28.1	799	20	AA86128	EST sequence for D
10	567.6	24.4	928	25	ABT32087	NOVX DNA sequence
11	527.4	22.6	777	25	ABT32088	NOVX DNA sequence
12	505.2	21.7	671	24	ABL89791	Human polynucleoti
13	372.4	16.0	669	22	AAF93972	Primer specific fo
14	251.8	10.8	3293	22	AAD06048	Human extracellular
15	248.6	10.7	2155	22	AAC84887	Human SEC6 nucleic
16	248.6	10.7	2156	22	AAC84892	Human SEC11 nucleic
17	248.6	10.7	2284	22	AAC84888	Human SEC7 nucleic
18	248.6	10.7	3556	22	AAD08283	Human secreted pro
19	248.6	10.7	3776	24	ABN83983	Human gene sequenc
20	247.8	10.6	2558	24	AAD28948	Human MOL5b cDNA.
21	247.8	10.6	3112	24	AAD28949	Human MOL5c cDNA.
22	247	10.6	3781	21	AAA37092	Human PRO1480 (UNQ
23	247	10.6	3781	22	AAS46151	Human DNA encoding
24	247	10.6	3781	22	AAF54381	Primer #75 used in
25	247	10.6	3781	25	ACA57909	Human PRO1480 cDNA
26	247	10.6	3781	25	ABX98379	Human cDNA encodin
27	247	10.6	3781	25	ABX98881	Novel human secret
28	247	10.6	3781	25	ACA05926	Human secreted/tra
29	247	10.6	3781	25	ABX97970	Human PRO polynuci
30	247	10.6	3781	25	ABX78754	Human PRO polynuci
31	247	10.6	3781	25	ABX75767	Human cDNA encodin
32	247	10.6	3781	25	ABX76972	Human PRO polynuci
33	247	10.6	3781	25	ABX16812	Human cDNA encodin
34	246	10.6	3868	24	AAD28947	Human MOL5a cDNA.
35	245.4	10.5	3503	22	AAF29461	Murine M-Sema-F CD
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37	245.4	10.5	3766	24	ABN83984	Human gene sequenc
38	245.4	10.5	3766	25	ACC51059	Human bladder canc
39	245.4	10.5	3766	25	ABX76369	Lung cancer-associ
40	238.4	10.2	8095	24	ABX92031	Lung specific nucl
41	238.4	10.2	8144	25	ABT13397	Breast specific re
42	238.2	10.2	2703	21	AAA47437	Sequence encoding
43	238	10.2	333	19	AAV07286	Human semaphorin W
44	228	9.8	2390	24	ABK11109	DNA encoding human
45	224.4	9.6	2615	24	ABQ99272	Human coding sequ

ALIGNMENTS

RESULT 1
AAV07280
ID AAV07280 standard; cDNA to mRNA; 2331 BP.
XX AAV07280;
AC AAV07280;
XX
DT 08-SEP-1998 (first entry)
XX
DE Rat semaphorin W encoding cDNA.
XX
KW Rat; semaphorin W; nerve extension inhibitor; antiallergic; anticancer;
KW immunosuppressant; gene therapy; diagnosis; research reagent; ds.
XX
OS Rattus norvegicus.
XX
FH Key Location/Qualifiers
FT CDS 1..2331
FT FT /*tag= a
FT FT /product= "semaphorin W"
XX
PN W09815628-A1.
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PD 16-APR-1998.
XX
PF 03-OCT-1997; 97WO-JP03549.
XX
PR 09-OCT-1996; 96JP-0287636.
XX (SUMU) SUMITOMO PHARM CO LTD.
XX Kikuchi K, Kimura T;
PI


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Db 1801 TGTGTGGGACCAGCCAGTGGAGTGACTCCGCTCACTCCCGGAGGGATGGACTAGAG 1860
Qy 1861 GTGTGTGAGCCAGGGGCGCATGGGGCTTATCTTGCAGTGTACAGAGGGTGGAGCC 1920
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RESULT 2

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XX
DT 08-SEP-1998 (first entry)
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DE Rat semaphorin W encoding cDNA with 5'UTR and 3'UTR.
XX
KW Rat; semaphorin W; nerve extension inhibitor; antiallergic; anticancer;
KW immunosuppressant; gene therapy; diagnosis; research reagent; ds.
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XX
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FT ET /*tag= b
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PD 16-APR-1998.
XX
PF 03-OCT-1997; 97WO-JP03549.
XX
PR 09-OCT-1996; 96JP-0287636.
XX
PA (SUMU ) SUMITOMO PHARM CO LTD.
XX
PI Kikuchi K, Kimura T;
XX
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DR WPI; 1998-261015/23.
DR P-PSDB; AAW51313.
XX Nerve extension inhibitor protein semaphorin W - is useful as
PT therapeutic drug and diagnostic and research reagent
XX
XX Claim 2; Page 55-57; 90pp; Japanese.
XX
CC The present sequence encodes rat semaphorin W. Semaphorin W and its
CC derivatives are nerve extension inhibitors which are useful as
CC antiallergic, immunosuppressant and anticancer agents. The DNA
CC encoding semaphorin W can also be used in gene therapy, e.g. using
CC a viral vector. The proteins, peptides, DNA and antibodies which
CC recognise the protein or peptides, can be used as diagnostic or
CC research reagents. Semaphorin W can be used as a screen for
CC semaphorin W antagonists with possible therapeutic use.
XX
SQ Sequence 4008 BP; 775 A; 1135 C; 1141 G; 957 T; 0 other;
Query Match 100.0%; Score 2331; DB 19; Length 4008;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 676 CTGGGGACTGAGCCCATCATCTCCGAGCTGTGGGTGAGCTGAGGACTGGATTCGAACA 735
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QY 1021 GGAGCTGCATCTCTGTGTGTGTGCTTCCGACCCCAAGACATCCGGGCACTGCTGAAT 1080
Db 1096 GGAGCTGCATCTCTGTGTGTGTGCTTCCGACCCCAAGACATCCGGGCACTGCTGAAT 1155
QY 1081 GGTCTCTTTAGAGAGCTAAACATGACTGCAACAGGGGACTGCTGTCTATGCACACGAG 1140
Db 1156 GGTCTCTTTAGAGAGCTAAACATGACTGCAACAGGGGACTGCTGTCTATGCACACGAG 1215
QY 1141 GTGCCCGCCAGACCTGGAGAGTGCATCGCAACAAACATGAAGCTCCAGAGTTTGA 1200
Db 1216 GTGCCCGCCAGACCTGGAGAGTGCATCGCAACAAACATGAAGCTCCAGAGTTTGA 1275
QY 1201 TCCTCACTCTCCTGCCAGACCGGTGTCTACCTTTATCAGAGACACCCCTCTCATGGAC 1260
Db 1276 TCCTCACTCTCCTGCCAGACCGGTGTCTACCTTTATCAGAGACACCCCTCTCATGGAC 1335
QY 1261 AGGCGCGTGTCCCGGCTGACGGCGCCCGCTGCTGCTACTACAGATACAGCTTATCTC 1320
Db 1336 AGGCGCGTGTCCCGGCTGACGGCGCCCGCTGCTGCTACTACAGATACAGCTTATCTC 1395
QY 1321 AGAGTCGTGGCCACAGAGGTGACACAGCCTCTCAGGGAAGAAATATGAGTGTCTACCTG 1380
Db 1396 AGAGTCGTGGCCACAGAGGTGACACAGCCTCTCAGGGAAGAAATATGAGTGTCTACCTG 1455
QY 1381 GGGCAGAGAGTGGACACTCCACCGGGGTGTGCGCATTTGGAGCTCAGTCTAGTCTTG 1440
Db 1456 GGGCAGAGAGTGGACACTCCACCGGGGTGTGCGCATTTGGAGCTCAGTCTAGTCTTG 1515
QY 1441 GAGGATCTGGCTTCTCCAGAACACAGCGGTTGAGAGCATGAATTTACACAGAT 1500
Db 1516 GAGGATCTGGCTTCTCCAGAACACAGCGGTTGAGAGCATGAATTTACACAGAT 1575
QY 1501 TGGCTCTCTGGTGGCTCCCATACTAGGTGACACAAGTGAACACCACTGTGGCGGT 1560
Db 1576 TGGCTCTCTGGTGGCTCCCATACTAGGTGACACAAGTGAACACCACTGTGGCGGT 1635
QY 1561 CTCAGAGTGTCTGGAGTGTATCTTGGCCAGGACCCCGTGTGCGCTGGAGCTTCCGG 1620
Db 1636 CTCAGAGTGTCTGGAGTGTATCTTGGCCAGGACCCCGTGTGCGCTGGAGCTTCCGG 1695
QY 1621 CTTGATGTCTGTGGCCACCGCCGCGAGCACCGCGGATGGTTCAAGATATAGATCA 1680
Db 1696 CTTGATGTCTGTGGCCACCGCCGCGAGCACCGCGGATGGTTCAAGATATAGATCA 1755
QY 1681 GCGGATGTCTCTTTTGTGTCAAAGAACTGGAGAACATCCCGTAGTGTGTTGAAGTT 1740
Db 1756 GCGGATGTCTCTTTTGTGTCAAAGAACTGGAGAACATCCCGTAGTGTGTTGAAGTT 1815
QY 1741 CCGGTGGCTACTGTGGGCCAGTGTCTGTCATGTTCCCGAGTTCTGCTGGGCATCC 1800
Db 1816 CCGGTGGCTACTGTGGGCCAGTGTCTGTCATGTTCCCGAGTTCTGCTGGGCATCC 1875
QY 1801 TGTGTGTGGCACCGCCAGTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1860
Db 1876 TGTGTGTGGCACCGCCAGTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1935

QY 1861 GTGGTGGTACCCAGGGGCCATGGGGGCTTATGCTTGGAGTGTTCAGAGGTGGAGCC 1920
Db 1936 GTGGTGGTACCCAGGGGCCATGGGGGCTTATGCTTGGAGTGTTCAGAGGTGGAGCC 1995
QY 1921 GCGCCGCTGGTGGCTGTATAGCTTGTGTGGGACAGCAGCGGGGACCTCAAAACGG 1980
Db 1996 GCGCCGCTGGTGGCTGTATAGCTTGTGTGGGACAGCAGCGGGGACCTCAAAACGG 2055
QY 1981 GCGCACACCGTGTGGGGCTGATTTGGTGGTGTCTCTCGGTGTTCTTCGACATCC 2040
Db 2056 GCGCACACCGTGTGGGGCTGATTTGGTGGTGTCTCTCGGTGTTCTTCGACATCC 2115
QY 2041 CTCACCTCTCTCTGATTGGTGGCTCAGCAGCTCGGCGACAGAGGGAGCTTCTAGCT 2100
Db 2116 CTCACCTCTCTCTGATTGGTGGCTCAGCAGCTCGGCGACAGAGGGAGCTTCTAGCT 2175
QY 2101 AGAGACAGAGTGGCTTAGATCTGGGGCTCCACCTTCTGGGACACACAGCTATAGTCAG 2160
Db 2176 AGAGACAGAGTGGCTTAGATCTGGGGCTCCACCTTCTGGGACACACAGCTATAGTCAG 2235
QY 2161 GACCCCTCTCTCTGCTTCCCTGAAGATGAACGGCTGCCCTGGGTAAGCGGGC 2220
Db 2236 GACCCCTCTCTCTGCTTCCCTGAAGATGAACGGCTGCCCTGGGTAAGCGGGC 2295
QY 2221 AGTGTGTTTGGTGGCTTCCCTCACCTTCTCTGCTGGATTTGCCCAGCCAGCCAC 2280
Db 2296 AGTGTGTTTGGTGGCTTCCCTCACCTTCTCTGCTGGATTTGCCCAGCCAGCCAC 2355
QY 2281 ATCCGGCTCACTGGGGCGCTCTAGCCAGCTGTGATGAGACCTCCATCTAA 2331
Db 2356 ATCCGGCTCACTGGGGCGCTCTAGCCAGCTGTGATGAGACCTCCATCTAA 2406

RESULT 3

AAZ87977
ID AAZ87977 standard; DNA; 4024 BP.

XX AAZ87977;

DT 05-JUN-2000 (first entry)

XX Mouse semaphorin W polypeptide encoding DNA.

XX Semaphorin W gene; hereditary disease; Parkinson's disease; mouse; ds.

OS Mus musculus.

FH Key Location/Qualifiers

FT CDS 79..2412

FT /*tag= a

PN WO200006725-A1.

XX 10-FEB-2000.

XX 30-JUL-1999; 99WO-JP04120.

PR 31-JUL-1998; 98JP-0217467.

PR 24-FEB-1999; 99JP-0046833.

XX (SUMU) SUNITOMO PHARM CO LTD.

XX Kimura T, Encinas JA;

XX WPI; 2000-195293/17.

DR P-PSDB; AAY77803.

XX Diagnosis of hereditary diseases such as Parkinson's disease by
PT analyzing the occurrence of mutation in the semaphorin W gene, or
PT determining the genotype of the semaphorin W gene in an individual
PS Disclosure; Page 22-28; 40pp; Japanese.

The invention provides a method for diagnosing or determining hereditary diseases by analyzing the occurrence of mutation in the semaphorin W gene. The semaphorin W gene is useful for the diagnosis of hereditary diseases such as Parkinson's, and for determining the genotype of the semaphorin W gene in an individual. The present sequence represents a semaphorin W mouse semaphorin W polypeptide.

Sequence 4024 BP; 768 A; 1128 C; 1172 G; 956 T; 0 other;

Query Match	91.8%	Score 2138.8;	DB 21;	Length 4024;
Best Local Similarity	95.1%	Pred. NO. 0;		
Matches 2219;	Conservative	0;	Mismatches	112; Indels 3; Gaps 1;

Qy	1	ATGCTTGCCAGGGCCGAGCGCCCCCGCCGGCCCCCGCGCGCTCCGGGTCTTTCCCTTC	60
Db	79	ATGTGCGCAGGGCCGAGCGCCCCCGCCGGCCCCCGCGCGCTCTCTCTCTCTCTCTC	138
Qy	61	CCGCGCGCGCTGTC--GCTGCTGCTGCTGCTGGCGGATACTAAGGCGCCCGGTGTGGCG	117
Db	139	CCGCGCGCGTGTGCTGCTGCTGCTGCGATGCTGAGCGGCCCGGTGTGGCGC	198
Qy	118	CGCTGCCCGCGCTCAGTGCCCGAGAACCTCGCTGCCCCATCTCCGAGGCTGACTCCCTATCTC	177
Db	199	CGCTGCCCGCGCTCGGTGCCAGAACCTCGCTGCCCCATCTCCGAGGCTGACTCCCTATCTC	258
Qy	178	ACCGGTTTGCAGGCTCTCATPACGTACAATTACTGTCTCTCTCTCTCTCTCTCTCTCTCT	237
Db	259	ACCGGTTTGGGCGCCCTCATACGTACAATTACTGTCTCTCTCTCTCTCTCTCTCTCTCT	318
Qy	238	CACACACTTACGTTCGCTGTCACGGGATAGCATCTTCGGTTTAAACCTCCCTCTCTCTGGG	297
Db	319	CACACACTTACGTTCGCTGTCACGGGACAGCATCTTCGGTTTAAACCTCCCTCTCTGGG	378
Qy	298	GAAGACCCGAAGGATCGACTGGATGGTACTTGAGACTCACAGACAGAACTGCAGGAAG	357
Db	379	GAAGACCTCGAAGGATCGACTGGATGGTGCCCGAGACTCACAGACAGAACTGTAGGAAG	438
Qy	358	AAAGCAAGAAAGAGGACGAATGTCACAATTTTATCCAGATTCTCGCCATTGTCAATGCC	417
Db	439	AAAGCAAGAAAGAGGACGAATGTCACAATTTTATCCAGATTCTCGCCATTGTCAATGCC	498
Qy	418	TCTCACCTCTCACGTGGGGCACCTTCGCTTTTGATCCGAAGTGGGGGTTATTGATGTG	477
Db	499	TCTCACCTCTCACGTGGGGCACCTTCGCTTTTGATCCGAAGTGGGGGTTATTGATGTG	558
Qy	478	TCCAGTTTCCAGCAGGTTGAAGACTTCAGAGCGCGCGGGGAATGTCTTTTGAGCCA	537
Db	559	TCCAGTTTCCAGCAGGTTGAAGACTTCAGAGTGGCCGGGGAATGTCTTTTGAGCCA	618
Qy	538	GCTCAACGGTCAGCAGCTGTAAATGGCTGGGGCGCTCTCTACACCGCCACTGTGAAGAC	597
Db	619	GCTCAACGGTCAGCAGCTGTAAATGGCTGGGGCGCTCTCTACACCGCCACTGTGAAGAC	678
Qy	598	TTCTCTGGGACTGAGCCCATCATCTCCGAGCTGTGGGTGAGCTGAGGATCGA	657
Db	679	TTCTCTGGGACAGACCGCATTTCTCCGAGCTGTGGGTGAGCTGAGGATTCGA	738
Qy	658	ACAGAGACCTTGTCATCTGCTTAATGCTCCAGCCTTTGTGCGAGCTATGGTCCTGAGC	717
Db	739	ACAGAGACCTTTGTCATCTGCTTAATGCCCCAGCCTTTGTGCGAGCTATGGTCCTGAGC	798
Qy	718	CCAGCTGAGTGGGGGATGAAGATGGAGACCATGAAATCTTTTTTCTTCCACGAGACC	777
Db	799	CCGCTGAGTGGGGGATGAAGATGGAGACCATGAAATCTTTTTTCTTCCACGAGACC	858
Qy	778	TCCCGAGTTTGGACTCTATGAGCGCATCAAGTTCCTCAAGAGTGGCCCGAGTGTGCGG	837
Db	859	TCCCGAGTCTGGACTCATATGAGCGCATCAAGTTCCTCAAGAGTGGCCCGTGTGTGCGG	918
Qy	838	GGGACCTTGGGGCAGGAAGACCTTCACGAGATGGACGACGTTTCTGAAGGCTGAC	897
Db	919	GGGACCTTGGGGCAGGAAGACCTTCACGAGATGGACGACGTTTCTAAAGGCTGAC	978

Db	868	CGAGCATTTGACATCATACGAGCGGATTAAGTCCCACGGGTGCGCGTGTGTGCGGGG	927
Qy	841	GACCTTTGGGGCCAGGAAGACCCCTTCAGCAGAGATGGACGACGTTTCTGAAGGCTGACCTG	900
Db	928	GACCTCGGGGCGCGGAACCCCTCCAGCAGAGATGGACGACGTTTTTGAAGCTGACCTG	987
Qy	901	CTGTGCCAGGGGCCGAGCATGCGCGGGCCCTCGGGGTTCGTGACGCTATGGCAGAGCTT	960
Db	988	CTCTGTCCAGGGCTGAGCATGGCGGGCTCCAGCTGTCTCGCAGGATGTTCGTGTGCTT	1047
Qy	961	CGGCTCAGCCTGGAGCGGAACCCCATCTTTATGGGATCTTTTCCCTCCCAGTGGAA	1020
Db	1048	CGACCTGAGCTTGGGCAGGAGATCCCATCTTTATGGCATCTTTCTTCCCAGTGGGAG	1107
Qy	1021	GGAGCTGCCATCTCTGTGTGTGCTTCCGACCCCAAGACATCCGGGCAGTGCAT	1080
Db	1108	GGGGCTACTATCTCTGTCTGTGCTTCCGACCACAAGACATTCGGACAGTGTCTGAAT	1167
Qy	1081	GGTCCCTTTAGAGACTAAACATGACTGCAACAGGGGACTGCTCTATGAGACAAACGAG	1140
Db	1168	GGTCCCTTCAGAAACTAAAACATGACTGCAACAGAGGACTGCTGTCTGTGGACAATGAT	1227
Qy	1141	GTGCCCCAGCCAGACCTTGAGAGTGCATCGCCAAACAATGAACTCCAGCAGTTTGGAA	1200
Db	1228	GTGCCCCAGCCAGACCTTGAGAGTGCATCACCACAACATGAAGTCCGGCACTTTGGC	1287
Qy	1201	TCCTCACTCTCCCTGCCAGACCGGTCTCACCTTTATCAGAGACCACTCTCATCTGGAC	1260
Db	1288	TCATCTCTCTCCCTGACCGGTACTCACCTTCATCCGGGACCACTCATCTGGAC	1347
Qy	1261	AGGCCCTGTTCGGGCTGACGGCGGCCCTGCTGGTCACTACAGATACAGCTATCTC	1320
Db	1348	AGCCAGTGTTCACAGCTGATGCCACCCCTGCTGGTCACTACAGATACAGCCTATCTC	1407
Qy	1321	AGAGTCTGGCCACAGGGTGACAGCCTCTCAGGGAAAGAATATGACGTGCTCTACCTG	1380
Db	1408	AGAGTCTGTGCCACAGGGTGACAGCCTCTCAGGGAAAGAGTATGATGTGCTCTACCTG	1467
Qy	1381	GGACAGAGATGGACACCTCCACGGGCTGCGGATTCGAGCTCAGCTCAGTCTGCTTG	1440
Db	1468	GGACAGAGATGGACACCTCCACCGAGCAGTGGGATCGGAGCTCAGCTCAGCGTCTT	1527
Qy	1441	GAGGATCTGGCTTGTTCAGAACCAACACAGCCGGTTGAGAGCATGAAATTTGATACCAGAT	1500
Db	1528	GAAGATCTGGCTTATTCACAGAGCCACAGCCAGTTGAGAACATGAAATTTGATACCAGC	1587
Qy	1501	TGGCTCTGTGGGCTCCCATATGAGGTGACACAAAGTGAACACCACTGAGTGGCCGT	1560
Db	1588	TGGCTCTGTGGCTCCGCTACTGAGGTGACACAAGTGAATACAACCACTGTGGCCGT	1647
Qy	1561	CTCCAGAGCTGCTCGGAGTGTATCTTGGCCCCAGGACCCCGTGTGCGCTGGAGCTTCCCG	1620
Db	1648	CTCCAGAGCTGCTCAGAGTGCATCTTGGCCCCAGGACCCAGTGTGCTGAGAGCTTCCCG	1707
Qy	1621	CTTGATCTGTGTGGCCACGCGGGGAGCACCGGGATGGTTCAAGATATAGAGTCA	1680
Db	1708	CTGGATCAGTGTGTGGCCCATGCCGGGAGCACCGAGGGTTGGTCCNAGACATAGAGTCA	1767
Qy	1681	CGGGATCTCTCTTTGTGTCCAAAAAGAACCTGGAGAACATCCCGTAGTGTTTGAAGTT	1740
Db	1768	GCAGATCTCTCTTTGTGTCTTAAAGAGCCTGGAGAACGTCACAGTAGTGTTTGAAGTT	1827
Qy	1741	CCGGTGGCTACTGTGGCCACAGTGGTCTTGGCATGTTCGCCAGTCTGCTCGGCACTCC	1800
Db	1828	CCGGTGGCTACAGCTGCGCATGTGGTCTTGCCATGTTCCTCAAGCTCAGCATGGGATCC	1887
Qy	1801	TGCTGTGGCACAGCCAGTGGAGTGACTGCGCTCACTCCCGGAGGGATGACATAGAG	1860
Db	1888	TGCTGTGGCACAGCCAGTGGAGTGACTGCACTACCCCGGCGGATGACATGGAG	1947
Qy	1861	GTGGTGTGACCCAGGGGCCATGGGGCTTATGCTTTCGAGTGTCTCAGGAGGTGGAGCC	1920

Db	1948	GTGTGGTGACCCACAGGGCCATGGGCGCTTATCCCTGTGTAATGTCAAGGAGGGTGGGGCA	2000		
Qy	1921	GCCGCGGTGGTGGCTTATAGCTTGGTGTGGGGCAGCCAGCGGGGACCCCTCAAAACGG	1980		
Db	2008	GCCCATGTGGTAGCAGCTTACAGCTTGGTATGGGGCAGCCAGCAGATGCTCCGAGCGG	2067		
Qy	1981	GCCACACACCGTGTGGGGCTGGATGGTGGGCTTTCTCTCTGGGTGTCTTTCGAGCATCC	2040		
Db	2068	CCCCACAC- --AGTGGGGGGGAGCTGGCTGGCTTCTTCTTGGGGATTCCTCGCAGCATCC	2124		
Qy	2041	CTCACTCTCCCTGATTGGTTCGCGCTCAGCAGCGTCGGGCACAGAGGGAGCTTCTAGCT	2100		
Db	2125	CTGACTCTCATCTTGATTTGGTGGCGCTCAGCAGCGACGGCGACAGAGGGAACTTCTGGCT	2184		
Qy	2101	AGAGACAAGGTGGGCTTAGATCTCTGGGGGCTCCACCTTCTGGGACCCACAAGCTATAGTCAG	2160		
Db	2185	AGAGACAAGGTGGGCTGGACCTGGGGCTCCACCTTCTGGGACCCACAAGCTACAGCAA	2244		
Qy	2161	GACCCCTCCCTCTCTCTGGCTGAAGATGAAGCGGTGCCCTGGCCCTGGGTAGCGGGGC	2220		
Db	2245	GACCCCTCCCTCCCTCTCTCTGAAGATGAAGCGGTGGCCCTGGCCCTGGCCAAAGAGGGGC	2304		
Qy	2221	AGTGGTTTTGGTGGCTTCCCTCCACCCCTTCTCTCTGGATTCTTCCGCAAGCCAGCCAC	2280		
Db	2305	AGTGGCTTTGGTGGATTCTTACCACCCCTTCTCTCTGGATTCTTCCGCAAGCCAGCCAC	2364		
Qy	2281	ATCCGGGCTCACTGGGGGGCCCTCTAGCCACGCTGTGATGAGACCTCCATCTA	2330		
Db	2365	ATTCGGCTAACTGGGGCTCTCTAGCCACATGTGATGAACATCCATCTA	2414		
RESULT 5					
AX	AX86126	AAAX86126 standard; DNA; 2893 BP.			
AC	AX86126;				
DT	15-SEP-1999	(first entry)			
DE	DNA encoding SBSEMN1, a semaphorin family polypeptide.				
KW	SBSEMN1; semaphorin; neurodegeneration; spinal injury; neuropathy;				
KW	neuromuscular disorder; muscular dystrophy; psychiatric disorder;				
KW	inflammatory disorder; developmental malformation;				
KW	immune system disorder; cancer; viral infection; vaccine; ss.				
OS	Homo sapiens.				
PN	EP033425-A1.				
PD	04-AUG-1999.				
PF	30-SEP-1998; 98EP-0203287.				
PR	30-JUL-1998; 98GB-0016676.				
PR	30-JAN-1998; 98EP-0300693.				
PR	28-JUL-1998; 98GB-0016423.				
PA	(SMK) SMITHKLINE BEECHAM PLC.				
PI	Doe TR, Hayes PD, Michalovich D;				
DR	WPI; 1999-407151/35.				
DR	P-PSDB; AAY23873.				
PT	New semaphorin family polypeptide useful for treating spinal injury				
PT	and muscular dystrophy				
PS	Claim 7; Page 13-14; 29pp; English.				
CC	The present sequence encodes SBSEMN1, a semaphorin family polypeptide.				
CC	The polypeptide may be used to screen for agonists or antagonists				
CC	including antibodies. Measurement of the level of SBSEMN1 protein				

Db	1916	GCCCATGTGTTAGACGGCTTACAGCTTGTTGGTATGGGGCAGCACCGAGATGCTCCGAGGCCGG	1976
Qy	1981	GCCCACACCCTTTGTGGGGGCTGGATTGGTTGGCTTTTCCTCTGGGTGTTCTTGTTCGAGCATCC	2040
Db	1976	GCCCCACAC---AGTGGGGGGGACTGGCTGGCTTCTTCTTTGGGGATTCTTCGAGCATCC	2032
Qy	2041	CTCACTCTCTCTCTGATTGGTTCGCCGCTCAGCAGCGTCCGGGCAGAGGGAGCTTCTTAGCT	2100
Db	2033	CTGACTCTCATTTCTGATTGGTTCGGCGCTCAGCAGCGACGGCGACAGAGGAACCTTCTGGCT	2092
Qy	2101	AGAGACAAGGTGGGCTTAGACTCTGGGGCTCCACCTTCTGGGACCACAAAGCTATAGTCAG	2160
Db	2093	AGAGACAAGGTGGGCTGGACCTTGGGGCTCCACCTTCTGGGACCACAAAGCTACAGCCAA	2152
Qy	2161	GACCCCTCCCTCTCTTTCGCCCTGAAGATGAACGGCTGCCCTCGGCCCTGGGTAAAGCGGGC	2220
Db	2153	GACCCCTCCCTCCCTCTCTCTGAAGATGAGCGGTTGCCGCTGGCCCTGGCCAAGAGGGGC	2212
Qy	2221	AGTGGTTTTGGTGGCTTCCCTCCACCCCTTCTCTGCTGATTTTGGCCCAAGCCAGCCCCAC	2280
Db	2213	AGTGGCTTTGGTGGATTCTCACCACCCCTTCTCTGCTTGATCTTGGCCCAAGCCAGCCCCAC	2272
Qy	2281	ATCCGGCTCACTGGGGCGCTCTAGCCACGTGTGATGAGACCTCCCATCTA	2330
Db	2273	ATTCGGCTAACTGGGGCTCTCTAGCCACATGTGATGAACATCCATCTA	2322
 RESULT 6 AAx86127			
ID	AAx86127 standard; DNA; 2894 BP.		
XX	AAx86127;		
XX	15-SEP-1999 (first entry)		
DT			
DE	EST sequence for DNA encoding SBSEMN1.		
KW	SBSEMN1; semaphorin; neurodegeneration; spinal injury; neuropathy;		
KW	neuromuscular disorder; muscular dystrophy; psychiatric disorder;		
KW	inflammatory disorder; developmental malformation; EST;		
KW	expressed sequence tag; immune system disorder; cancer;		
KW	viral infection; vaccine; ss.		
OS	Homo sapiens.		
PN	EP933425-A1.		
PD	04-AUG-1999.		
Pf	30-SEP-1998; 98EP-0203287.		
PR	30-JUL-1998; 98GB-0016676.		
PR	30-JAN-1998; 98EB-0300693.		
PR	28-JUL-1998; 98GB-0016423.		
XX	(SMIK) SMITHKLINE BEECHAM PLC.		
XX	Doe TR, Hayes PD, Michalovich D;		
PI			
XX	WFI; 1999-407151/35.		
DR	P-PSDB; AAY23874.		
XX			
PT	New semaphorin family polypeptide useful for treating spinal injury		
PT	and muscular dystrophy		
XX			
PS	Claim 18; Page 14-15; 29pp; English.		
XX			
CC	The present sequence represents an expressed sequence tag (EST)		
CC	sequence, from which DNA encoding SBSEMN1, a semaphorin family		
CC	polypeptide, is derived. The polypeptide may be used to screen		
CC	for agonists or antagonists including antibodies. Measurement		
CC	of the level of SBSEMN1 protein and detection of a mutation in		
CC	its polynucleotide may also be used to diagnose a disease or		

FH	Key	Location/Qualifiers
FT	CDS	1..1764
FT		/*tag= a
FT		/product= "semaphorin W"
XX	WO9815628-A1.	
XX	16-APR-1998.	
XX	03-OCT-1997;	97WO-JP03549.
XX	09-OCT-1996;	96JP-0287636.
XX	(SUMU)	SUMITOMO PHARM CO LTD.
XX	Kikuchi K,	Kimura T;
DR	WPI;	1998-261015/23.
DR	P-PSDB;	AAW51314.
XX	Nerve extension inhibitor protein semaphorin W - is useful as therapeutic drug and diagnostic and research reagent	
XX	Claim 2;	Page 67-68; 90pp; Japanese.
XX	The present sequence encodes human semaphorin W. Semaphorin W and its derivatives are nerve extension inhibitors which are useful as anti-allergic, immunosuppressant and anticancer agents. The DNA encoding semaphorin W can also be used in gene therapy, e.g. using a viral vector. The proteins, peptides, DNA and antibodies which recognise the protein or peptides, can be used as diagnostic or research reagents. Semaphorin W can be used as a screen for semaphorin W antagonists with possible therapeutic use.	
XX	Sequence	1761 BP; 349 A; 511 C; 521 G; 380 T; 0 other;
QY	Query Match	59.7%; Score 1391.2; DB 19; Length 1761;
DB	Best Local Similarity	87.2%; Pred. No. 0;
QY	Matches	1538; Conservative 0; Mismatches 223; Indels 3; Gaps 1;
DB	565	GGGGCGTCTCTACACGCCACTGTGAAGAACTTCTGGGGAGTGGCCCATCATCTCC 624
QY	1	GGGGGTGCTCTATGCTGCCACTGTGAAAACCTACCTGGGGACGGCAATTATCACC 60
DB	625	CGAGCTGGTGGTGGAGCTGAGGACTGGATTGCAACAGACAGACCTTGTTCATCTGGCTTAAT 684
QY	61	AGAGCAGTGGGTGCTGCCAGGACTGGATTTCGACAGATACCTTGCCTTCTTGGCTGAAC 120
DB	685	GCTCCAGCCTTTGTGCGACGCTATGTCCTGAGCCAGCTGAGTGGGGGATGAAGATGGA 744
QY	121	GCCCCAGCCTTTGTGCGACGCTGGCCTTGAGCCAGCCGAATGGGGGATGAAGATGGA 180
DB	745	GACGATGAATCTTTTTTCTTCAGGAGACCTCCGAGTGTGTGGACTCTTATGAGCGC 804
QY	181	GACGAGAAATCTACTTCTTTACGGAGACTTCCCGAGCATTTGACTCATACGAGCGC 240
DB	805	ATCAAGTCCCAAGAGTGGCCGAGTGTGGGGGACCTTGGGGCAGGAGACCCCTT 864
QY	241	ATTAAGTCCCAAGGTTGGCCGCTGTGTGGGGGGACCTCGGGGGCGGAAGACCCCTC 300
DB	865	CAGCAGAGATGGACGACGTTTCTGAAGGCTGACCTGTGTGCCAGGGCCCGAGCATGGC 924
QY	301	CAGCAGAGATGGACGACGTTTGAAGCTGACCTGTGTGCCAGGGCCCTGAGCATGGC 360
DB	925	CGGGCCTCCGGGTCTTCAGAGCTATGCGAGACTTCGGCCTCAGCCTCGAGCGGGAACC 984
QY	361	CGGGCCTCCAGTGTCTCGAGGATGTGCTGTGCTTCGACCTGAGCTTGGGGCAGGACT 420
DB	985	CCCATCTTTATGGGATCTTTCTCCAGTGGGAGGAGCTGCCATCTCTGCTGTGTGT 1044
QY	421	CCCATCTTTATGGGATCTTTCTTCCAGTGGGAGGAGCTTATCTCTGCTGTGTGT 480
QY	1045	GCCTTCCGACCCCAAGACATCCGGGCGAGTGTGTAATGGTCCCTTTTAGAGAGCTTAAACAT 1104

DB	481	GCCTTCCGACCAACAGACATTCGGACAGTGTCTGAATGGTCCCTTCAGAGAACTAAACAT	540		
QY	1105	GACTGCAACAGGGGACTGCTGTATGGACAACAGAGTGGCCCGCCAGCCAGACCTGGAGAG	1164		
DB	541	GACTGCAACAGAGGACTGCTGTCTGGACAATGATGTGCCCGCCAGCCAGACCTGGAGAG	600		
QY	1165	TGCATCGCCCAACACATGAAGCTCCAGAGTTTGGATCTCTCACTCTCCCTGCCAGACCGC	1224		
DB	601	TGCATCACCACCAACATGAAGCTCCGCGACTTTGGCTCATCTCTCTCCCTGCCAGACCGC	660		
QY	1225	GTGCTCACCTTTATCAGAGACACCTCTCATGGAAGGCCCTGTGTCGGGGTGAGCGG	1284		
DB	661	GTACTCACCTTTCATCGGGGACCACTCATGAGAGGCCAGTGTTCAGAGCTGATGGC	720		
QY	1285	CGCCCTCTGCTGCTCACTACAGATACAGCTATCTCAGAGTCTGTGCCCCACAGGGTGACC	1344		
DB	721	CACCCCTCTGCTGCTCACTACAGATACAGCTATCTCAGAGTCTGTGCCCCACAGGGTGACC	780		
QY	1345	AGCCTCTCAGGAAAGAATATGACGTGCTCTACCTGGGACAGAGATGACACCTCCAC	1404		
DB	781	AGCCTCTCAGGAAAGAGATGATGATGCTCTACCTGGGACAGAGATGACACCTCCAC	840		
QY	1405	CGGGCTGCTGCGATTTGGAGCTCAGCTCAGTGTCTTGGAGATCTGGCCTTTGTCAGAA	1464		
DB	841	CGAGCAGTGGGATCGGAGCTCAGCTCAGCGTTCTTTGAAGATCTGGCCTTATTTCCAGAG	900		
QY	1465	CCACAGCCGTTTGAGAGCATGAAATGTATCCAGGATTGCTCTGTGGGCTCCCATACT	1524		
DB	901	CCACAGCCAGTTTGAGAACATGAAATGTATCCAGCAGTGGCTCTGTGGTCCCTGCTACT	960		
QY	1525	GAGGTGACACAAAGTGAACACCAGCAACTGTGCCGCTCTCCAGAGCTGCTCGGAGTGTATC	1584		
DB	961	GAGGTGACACAAAGTGAATACAACTGTCGCGCTCTCCAGAGCTGCTCAGAGTGCATC	1020		
QY	1585	CTGGCCAGGACCCGCTGTGGCCTGGAGCTTCCGGCTTGTGCTGTGGCCACAGCC	1644		
DB	1021	CTGGCCAGGACCCAGCTGTGCTGTGGAGCTTCCGGCTGGATGTGTGGCCCTATGCC	1080		
QY	1645	GCGAGACCCGCGGATGTTCAAGATATAGAGTACGCGGATGCTCTCTTTGTGTCTCA	1704		
DB	1081	GGGGAGCAGCGAGGTTGGTCCAGACATAGAGTACAGAGATGTCTCTCTTTGTGTCT	1140		
QY	1705	AAAGAACCTGGAGAACATCCCGTAGTGTGTTGAAGTTCCGGTGGCTACTGTGGGCCACGTG	1764		
DB	1141	AAAGAGCCTGGAGAACCTCCAGTAGTGTGTTGAAGTTCCCGTGGCTACAGCTGCGCATGTG	1200		
QY	1765	GTCTTGCCATGTTCCCAAGCTCAGCATGGGCTCCTGTGTGGCACCCAGCTGGA	1824		
DB	1201	GTCTTGCCATGTTCCCAAGCTCAGCATGGGCTCCTGTGTGGCACCCAGCTGGA	1260		
QY	1825	GTGACTGCGCTCACCTCCCGAGGAGTGGACTAGAGTGGTGGTACCCAGCGGGCCATG	1884		
DB	1261	GTGACTGCGCTCACCTCCCGAGGAGTGGACTAGAGTGGTGGTGGTACCCAGCGGGCCATG	1320		
QY	1885	GGGGCTTATGCTTGGAGTGTCCAGAGGTGAGCGCCCGCGGTGGTGGCTGCTTATAGC	1944		
DB	1321	GGCGCTTATGCTGCTGAATGTCCAGAGGTGGGGGACCATGTGTAGCAGCTTACAGC	1380		
QY	1945	TTGGTGTGGGCGAGCGGGGACCTCAAAACGGGGCCACACCGTGTGGGGGCTGGA	2004		
DB	1381	TTGGTGTGGGCGAGCGAGATGCTCCGAGCCCGGGGCCACAC --- AGTGGGGGCGGA	1437		
QY	2005	TTGGTGTGGCTTCTCTGGGTGTTCTTGCAGCATCCCTCAGCTCTCTCTGATTGGTCCG	2064		
DB	1438	CTGGCTGGCTTCTCTTGGGATTCGCGAGATCCCTCAGCTCTCATCTGATTGGTCCG	1497		
QY	2065	GCTCAGCAGCTGCGCGAGCAGAGGAGCTTCTAGCTAGAGACAAGTGGGCTTAGATCTG	2124		
DB	1498	CGTACGACGCGACGCGAGAGGGAAGTCTTGGCTAGAGACAAGTGGGCTGGACCTG	1557		
QY	2125	GGGGCTCCACCTTCTGGGACCCACAGCTATAGTCAGGACCCCTCCCTCTCTCTCGCTGAA	2184		

PF 03-JUL-2002; 2002WO-US21360.
XX
PR 05-JUL-2001; 2001US-303046P.
PR 11-JUL-2001; 2001US-304502P.
PR 12-JUL-2001; 2001US-305011P.
PR 17-JUL-2001; 2001US-306089P.
PR 04-OCT-2001; 2001US-326981P.
PR 28-FEB-2002; 2002US-360923P.
PR 12-MAR-2002; 2002US-363636P.
PR 16-APR-2002; 2002US-373063P.
PR 02-JUL-2002; 2002US-0188246.
XX
PA (CURA-) CURAGEN CORP.
XX
XX Anderson DW, Boldog FL, Casman SJ, Edinger SR, Gerlach VL;
PI Gorman L, Li L, Malyankar UM, Patturajan M, Payman JA, Shenoy SG;
PI Shmkets RA, Vernet CAM, Voss EZ;
XX
DR WPI; 2003-221591/21.
DR P-PSDB; ABJ37120.
XX
XX New isolated NOVX polypeptides and polynucleotides, useful for
PT diagnosing, preventing or treating NOVX-associated disorders, e.g.
PT atherosclerosis, cancer, AIDS, Parkinson's disease, multiple sclerosis
PT or Alzheimer's disease -
XX
PS Claim 20; Page 97; 184pp; English.
XX
XX The invention relates to an isolated NOVX polypeptide comprising any of
CC 12, 83-450 residue amino acid sequences, given in the specification, a
CC mature form of the amino acids, a sequence at least 95 % identical to the
CC amino acids, or a sequence comprising one or more conservative
CC substitutions in the amino acids. The NOVX polypeptides are useful in
CC manufacturing a medicament for treating a syndrome associated with a
CC human disease, which is a pathology associated with the NOVX polypeptide.
CC The NOVX polypeptides, nucleic acids and antibodies are useful for
CC diagnosing, preventing or treating diseases such as atherosclerosis,
CC hypertension, cancer, tuberculous sclerosis, Alzheimer's disease,
CC Parkinson's disease, multiple sclerosis, cachexia, anorexia, obesity,
CC infertility, atherosclerosis, hypertension, scleroderma, haemophilia,
CC dyslipidaemias, diabetes, autoimmune disease, immunodeficiencies, AIDS,
CC or graft-versus-host disease. The nucleic acids are useful as
CC hybridisation probes, in chromosome mapping, tissue typing, preventive
CC medicine, or pharmacogenomics. This polynucleotide sequence represents
CC the coding DNA of a NOVX protein of the invention.
XX
SQ Sequence 777 BP; 153 A; 230 C; 208 G; 186 T; 0 other;

Query Match 22.6%; Score 527.4; DB 25; Length 777;
Best Local Similarity 90.2%; Pred. NO. 1.5e-125;
Matches 564; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 118 CGCGTCCCGCTCAGTCCCGCAGAACCTCGCTGCCCATCTCGAGGCTGACTCTATCTC 177
DB 7 CGCGTCCCGCTCAGTCCCGCAGAACCTCGCTGCCCATCTCTGAGGCTGACTCTGCTC 66
QY 178 ACCCGGTTGCGAGCGCTCTCATAGGTACAAATTAATCTGCTCTCTGCTGATCTCCGCC 237
DB 67 ACCCGGTTGCGAGCGCTCTCATAGGTACAAATTAATCTGCTCTCTGCTGATCTCCGCC 126
QY 238 CACACATTTACGTGGTGCACGGGATGACATCTTCGCTTTAAACCCCTCCCTTCTCTGGG 297
DB 127 CACACATTTATGTTGGCGCCGGGACACACCATCTTCGCTTTATCCCTGCCCTTCTCAGG 186
QY 298 GNAAGACCCCGAGGATCGATGGATGATGATGATGATGATGATGATGATGATGATGATG 357
DB 187 GAGAGACCCCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 246
QY 358 AAAGCAAGAAG 417
DB 247 AAAGCAAGAAG 306
QY 418 TCTACCTCTCTACGTGGCGGACACCTTCGCTTTTGTATCCGGAAGTGCGGGGTTATTGATG 477

Db 307 TCTCACCTCTCACTTGTGGCACCTTGGCTTTTGTATCCGAAGTCCGGGTTATTGATGTG 366
QY 478 TCCAGTTTCCAGCAGAGTTGAAAGACTTGAGAGCGCGCGGGAATGTCCCTTTTGAGCCA 537
Db 367 TCCAGTTTCCAGCAGAGTTGAAAGACTTGAGAGTGGCGGGAATGTCCCTTTTGAGCCA 426
QY 538 GCTCAACGGTCCAGCAGCTGTAATGGCTGGGGCGTCTCTACACGCCACTGTGAAGAAC 597
Db 427 GCTCAGCGTCCAGCAGCTGTAATGGCTGGGGGTGCTCTATGCTGCCACTGTGAAGAAC 486
QY 598 TTCTGGGGAGTGAAGCCATCATCTCCGAGCTGTGGTTCGAGCTGAGGACTGATTCGA 657
Db 487 TACCTGGGAGCGGAGCCAAATATCACCAGAGCAGTGGTCTGTCGCGAGGACTGATTCGG 546
QY 658 ACAGACAGCTTGTCTATCTCTGCTTAATGCTCCAGCTTTTTCGCGAGCTATGCTCCTGAGC 717
Db 547 ACAGATACCTTGTCTCTGCTGAAGCCCGCCCTTTGTTCGAGCGCTGCGCTTGAGC 606
QY 718 CCAGCTGAGTGGGGGATGAAGATG 742
Db 607 CCAGCGAATGGGGGATGAAGATG 631
RESULT 12
ABL89791
ID ABL89791 standard; cDNA: 671 BP.
XX
AC ABL89791;
XX
DT 24-MAY-2002 (first entry)
XX
DE Human polynucleotide SEQ ID NO 353.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200190304-A2.
XX
PD 29-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-US16450.
XX
PR 19-MAY-2000; 2000US-205515P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-122018/16.
XX
PT P-PSDB; ABB89382.
XX
PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive,
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
XX disorders -
PS Claim 4; SEQ ID NO 353; 2081pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABL89449-ABL90853) and proteins
CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune

CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 671 BP; 134 A; 176 C; 214 G; 140 T; 7 other;

Query Match 21.7%; Score 505.2; DB 24; Length 671;
Best Local Similarity 86.6%; Pred. No. 7.3e-120;
Matches 582; Conservative 7; Mismatches 80; Indels 3; Gaps 3;
QY 1312 GCCTATCTCAGAGTCGTGGCCACACAGGGTGACAGCCTCTCAGGGAAGAAATATGACGNG 1371
DB 1 GCCTATCTCAGAGTCGTGGCCACAC-GGTGACAGCCTCTCAGGGAAGAGTATGATGTG 59
QY 1372 CTCTACCTGGGACA-GAGGATGGACACCTCCACCGGCTGTCCGCAATGGAGCTCAGCT 1430
DB 60 CTCTACCTGGGACATGAGATGGACACCTCCACCGAGTCGCGATCGGAGCTCAGCT 119
QY 1431 CAGTGTCTGGAGGATCTGGCTTGTCCCAACACACAGCCGGTTGAGAGCATGAAT 1490
DB 120 CAGCGTTCTTGAAGATCTGGCCTTATTCACAG-AGCACAGCCAGTTGAGAATCAAT 178
QY 1491 GTACACAGATTGGCTCTCGTGGGTCCCATCTAGGTGACACAGTGAACACAGCAA 1550
DB 179 GTACACAGCTGGCTCTCGTGGTTCCTCGTACTGAGTGACACAAAGTGAATACAA 238
QY 1551 CTGTGGCCCTCTCCAGAGCTGCTCGGAGTGTATCTTGCCCAAGACCCCGTGTGGCCTG 1610
DB 239 CTGTGGCCCTCTCCAGAGCTGCTCAGAGTGCATCTGGCCAGGACCCAGTCTGTG 298
QY 1611 GAGCTTCCGGCTGTGCTGTGTGGCCACCGCCGAGCAGCCGGGATGGTTCAAGA 1670
DB 299 GAGCTTCCGGCTGTGATGTGTGGCCCATCCGGGGAGCACCAGGGGTGGTCCAAGA 358
QY 1671 TATAGAGTCAGGGGATGTCTCTTTGTGTCCAAAAGAACCTGGAGAACATCCCGTAGT 1730
DB 359 CATAGAGTCAGAGATGTCTCTCTTTGTGTCTTAAGAGCTTGAGACGTCCAGTAGT 418
QY 1731 GTTTGAAGTTCGGTGGCTACTGTGGGACACGTGTCTGCCATGTCCCCAGTTCGTGC 1790
DB 419 GTTTGAAGTTCGGTGGCTACTGAGTGCAGTGTGTGTGGCATGTCTTCCAAAGCTCAGC 478
QY 1791 CTGGGCATCTCTGTGTGCACACAGCCAGTGGAGTGTGCTGCTCACTCCCGGAGGA 1850
DB 479 ARGGGCAKCTGTGTGTGGCACACAGCCAGTGGAGTGAATGCAITCAMCCCCCGGGGA 538
QY 1851 TGGACTAGAGTGGTGGTGACCCAGGGGCCATGGGGCTTATGCTTGGAGTGTCAAGGA 1910
DB 539 TGGACTGAGTGGTGGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 598
QY 1911 GGGTGGAGCCGCCCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1970
DB 599 GGGTGGGAGCCCATGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 658
QY 1971 CTCAAACCGGC 1982
DB 659 TCCGAGCCGGC 670

RESULT 13
AAF93972
ID AAF93972 standard; DNA; 669 BP.
XX
AC AAF93972;
XX
DT 23-MAY-2001 (first entry)
XX

DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 406.
XX Human; secretory protein; membrane protein; vaccine; gene therapy;
KW rheumatoid arthritis; diabetes; PCR primer; ss.
XX Synthetic.
OS
PN EP1067182-A2.
XX
PD 10-JAN-2001.
XX
PF 07-JUL-2000; 2000EP-0114090.
XX
PR 08-JUL-1999; 99JP-0194179.
PR 11-JAN-2000; 2000JP-0118775.
PR 02-MAY-2000; 2000JP-0183766.
XX
XX (HELI-) HELIX RES INST.
PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX WPI; 2001-093989/11.
DR
XX
XX Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT gene therapy or as candidate target molecules in drug development -
XX
XX Claim 4; SEQ ID 406; 609pp + CD ROM; English.
XX
CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC which encode human secretory or membrane proteins represented by
CC AAF88317 - AAF88419. Included in the invention are primers
CC .AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
CC cDNA sequences of the invention. The invention also includes methods for
CC the production of antibodies directed against the proteins, and cDNA
CC sequences, which can be used in vaccines. The polynucleotide sequences
CC can be used in gene therapy. The polynucleotide sequences and the
CC proteins they encode may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate secretory
CC protein/membrane protein expression. The nucleic acids and complementary
CC sequences may also be used as DNA probes in diagnostic assays
CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
CC presence of similar nucleic acid sequences in samples. They may also be
CC used to study the expression and function of secretory proteins/membrane
CC polypeptides and their role in metabolism. The polypeptides may be used
CC as antigens in the production of antibodies against them and in assays to
CC identify modulators (agonists and antagonists) of expression and
CC activity. The antibodies (agonists and antagonists) may also be used as therapeutic
CC agents to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of the
CC polypeptides in samples (e.g. by enzyme linked immunosorbent assay
CC (ELISA)). Examples of diseases which may be treated include rheumatoid
CC arthritis and diabetes.
XX
SQ Sequence 669 BP; 119 A; 214 C; 179 G; 147 T; 10 other;

Query Match 16.0%; Score 372.4; DB 22; Length 669;
Best Local Similarity 80.0%; Pred. No. 1.1e-85;
Matches 463; Conservative 0; Mismatches 100; Indels 16; Gaps 2;
QY 1 ATGCTTGCAGGGCCGAGGGCCCGCCCGGGCCCGCCCGCCCTCCGGTCTTTCCCTTC 60
DB 102 ATGCCGGCTCTGCTGCGCGCCCGCCCGGGTCCCGGCGACCTACAGCTTCGGCTTC 161
QY 61 CCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 162 CC-----GCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 206
QY 121 GTCCCCCGCTCAGTCCCGACAGAACCTCGCTGCGCCATCTCCGAGGCTGACTTCCTAC 180
DB 207 GTCCCCCGCTCGGTGCCAGAACCTCGCTTCCAATCTCTGAGGCTGACTTCCTGCTC 266
QY 181 CGGTTTGCAGCTCTCATCATGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240

Db 267 CGGTTCCAGCTCCCTCACACATACAATTAATCTGTTCTCTCTGTTGATCTGCTGCCCTCCAC 326

Qy 241 ACACCTTTACGTCGGTCACGGGATAGCATCTTGGCTTTAACCTCCCTCTCTCTGCGGAA 300

Db 327 ACACCTTTATGTTGGCGCCGGACACATCTTGCCTTTATCCCTGCCCTTCTCAGGGAG 386

Qy 301 AGACCCCGAAGGATCGACTGGATGGTACCTGAGACTCACAGACAGAACTCCAGAGAAA 360

Db 387 AGACCCCGCANGATTGACTGGATGGTTCCTGANGCTCACANACAGAACTGTAGGAAGAA 446

Qy 361 GGCAAGAAAGACGACGAATCTCAATTTTATCCAGATCTCGCCATTGTCAATGCTCT 420

Db 447 GGCAAGAAAGACGAATCTCAATTTTGTCCAGATCTCGCCATTGTCCCAATGCTCT 506

Qy 421 CACCTCTCAGTCGCGCACCTTCGCTTTTGTATCCG-AAGTGGGGGTTATTGATGTGTC 479

Db 507 CACCTCTCACTTGTGCACCTTCGCTTTTGTATCCGAAATGCGGGTATTGATGTGTC 566

Qy 480 CAGTTTCCACAGGTTGAAGACTTGAGACGGCGGGGGAATGCTCTTTTGGCCAGC 539

Db 567 CAGGTTCCCGNGGTTGAAAACCTTGAATATGNGCGGGGGAATGCTCTTTGAACCACT 626

Qy 540 TCAACGGTCAGAGCTGTAATGCTGGGGCGTCTCTA 578

Db 627 CNGGTCANCACTTGTATTGCTGGGGGGTCTNTA 665

RESULT 14

AAD08048

ID AAD08048 standard; cDNA; 3293 BP.

XX AC AAD08048;

DT 06-AUG-2001 (first entry)

DE Human extracellular matrix and cell adhesion molecule-4 (XMAD-4) cDNA.

XX Human; extracellular matrix and cell adhesion molecule; XMAD;

KW gene therapy; genetic disorder; adrenoleukodystrophy; leukaemia;

KW Down's syndrome; cystic fibrosis; Gaucher's disease; myotonic dystrophy;

KW sickle cell anaemia; thalassaemia; autoimmune disorder; adenocarcinoma;

KW inflammatory disorder; acquired immune deficiency syndrome; AIDS;

KW Addison's disease; allergy; anaemia; asthma; atherosclerosis; melanoma;

KW Crohn's disease; diabetes mellitus; atopic dermatitis; lymphoma; cancer;

KW glomerulonephritis; multiple sclerosis; Grave's disease; osteoarthritis;

KW osteoporosis; psoriasis; rheumatoid arthritis; ulcerative colitis;

KW infection; cell proliferative disorder; actinic keratosis; myeloma;

KW arteriosclerosis; neutropenic; anticonvulsant; antithyroid; nephrotropic;

KW neuroprotective; dermatological; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

PH 134..2635

FT CDS /*tag= a

FT /product= "Human extracellular matrix and cell adhesion

FT molecule (XMAD)"

FT 134..202

FT sig_peptide /*tag= b

FT 203..2632

FT mat_peptide /*tag= c

FT /product= "Mature human extracellular matrix and cell

FT adhesion molecule (XMAD)"

XX W0200142285-A2.

XX PN 14-JUN-2001.

XX PD 05-DEC-2000; 2000WO-US32990.

XX PF 10-DEC-1999; 99US-0172852.

XX PR 16-DEC-1999; 99US-0172354.

XX

PA (JNCY-) INCYTE GENOMICS INC.

XX Yue H, Tang YT, Lal P, Burford N, Azimzai Y, Patterson C;

PI Baughn MR, Lu DAM, Shah P, Au-Young J;

XX WPI; 2001-381632/40.

DR P-PSDB; AAE03640.

XX New human extracellular matrix and cell adhesion molecules and

XX polynucleotide sequences encoding them, useful for diagnosis,

PT prevention, treatment of genetic, autoimmune and cell proliferative

PT disorders

XX Claim 5; Page 121-122; 135pp; English.

XX The present cDNA sequence encodes human extracellular matrix and cell

XX adhesion molecule (XMAD). The XMAD is used for screening a compound for

CC effectiveness as an agonist or antagonist of XMAD. The identified agonist

CC or antagonist are used for treating a disease or condition associated

CC with decreased or increased expression of functional XMAD. The

CC polynucleotides encoding XMAD are useful in somatic or germline gene

CC therapy to correct a genetic deficiency, to express a conditionally

CC lethal gene product and to express a protein which affords protection

CC against intracellular parasites and also for diagnosis of disorders

CC associated with expression of XMAD. They are also used for generating

CC hybridisation probes useful in mapping the naturally occurring genomic

CC sequences and to create knock in humanised animals (pigs) or transgenic

CC animals (mice or rats) to model human diseases. Oligonucleotide or longer

CC fragments derived from the polynucleotide sequences may be used as

CC elements on a microarray. Antibodies which specifically bind XMAD may be

CC used for the diagnosis of disorders associated with the expression of

CC XMAD, or in assays to monitor patients being treated with XMAD. Diseases

CC diagnosed, prevented or treated include genetic disorders such as

CC adrenoleukodystrophy, Down's syndrome, cystic fibrosis, Gaucher's

CC disease, myotonic dystrophy, sickle cell anaemia, thalassaemia,

CC autoimmune/inflammatory disorders such as acquired immune deficiency

CC syndrome (AIDS), Addison's disease, allergies, anaemia, asthma,

CC atherosclerosis, Crohn's disease, diabetes mellitus, atopic dermatitis,

CC glomerulonephritis, multiple sclerosis, Grave's disease, osteoarthritis,

CC osteoporosis, psoriasis, rheumatoid arthritis, ulcerative colitis,

CC bacterial, fungal, parasitic, protozoal and helminthic infections and

CC cell proliferative disorders such as actinic keratosis, arteriosclerosis

CC and cancer including breast, bladder, bone marrow, brain and uterus

CC cancer, leukaemia, adenocarcinoma, lymphoma, melanoma and myeloma.

XX SQ Sequence 3293 BP; 599 A; 978 C; 1052 G; 664 T; 0 other;

Query Match 10.8%; Score 251.8; DB 22; Length 3293;

Best Local Similarity 52.3%; Pred. No. 2.3e-54;

Matches 706; Conservative 0; Mismatches 627; Indels 18; Gaps 6;

Qy 308 GAAGGATCGACTGGATGGTACCTGAGACTCACAGACAGAACTCGAGGAAGAAAGGCAAG- 366

Db 387 GAGCGATCTCTCTGGGAGGCCCGCTGGAGAGAGAGACTGATGTATCCAGAAAGGGAAGA 446

Qy 367 --AAAGAGGACGAATGTCAAAATTTTATCCAGATTTCTGCCATTTGTCAATGCCCTCTCACC 424

Db 447 ACAACACAGACCGAGTGTCTCAACTTCTCCGCTTCTCCAGAGCCCTACAAATGCCCTCCACC 506

Qy 425 TCCTCAGTGGCGCACCTTCGCTTTTGTATCCGAGTGGGGGTTATTGATGTGTCCAGTT 484

Db 507 TGTACGCTCTGGCGACCTACGCTTCCAGGCCCAAGTGCACCTAGTCAACATGCTCACCT 566

Qy 485 TCCA---GCAGTTGAAAGACTTTCAGAGCGCGCGGGGAAATATTCCTTTTTCGAGCAGCTC 541

Db 567 TCACCTTTGGAGATGGAGATTTCAGATGGGAGGCAAGTGTCCCTATGACCCAGCTA 626

Qy 542 AACGGTCAGCAGCTGTATATGGCTGGGGCGCTCTCTACACCGGCACACTGTGAAGAACTTCC 601

Db 627 AGGSCCATGCTGGCCTTCTTTGTGGATGGTGAAGTGTACTCGGCCACACTCAACAACCTCC 686

Qy 602 TGGGGACTGAGCCCATCATCTCCGAGCTGTGGGTCGAGCTGAGGATGATTCGACACAG 661

Db 687 TGGGACCGAACCCATTATCTCGGTACATGGGCG---CCACCACTCCATGAAGACAG 743
QY 652 AGACCTTGTCATCTCGGCTTAATGCTCCAGCCTTTGTGCGAGCTATGCTCTGTGAGCCACG 721
Db 744 AGTACCTGGCCTTTTGGCTCAAGAACCTCACTTGTAGGCTCTGCCTATGTACCTGAGA 803
QY 722 CTGAGTGGGGGATGAAGATGAGACGATGAATATTTTTCCTACGAGACCTCC 781
Db 804 CTGTGGGAGCTTCAAGGGGACGACGACAAAGTCTACTTCTTTCAGGAGCGGGCAC 863
QY 782 GAGTCTTGACCTCTATGAGCGCATCAAGTCCCAAGAGTGGCCGAGCTGTGTGGGGG 841
Db 864 TGGAGTCCGACTGCTATCCGAGCAGGTGGTCTGTGTGGCCGCTGTGCGAAGGGCG 923
QY 842 ACCTTTGGGGGAGGAGACCTTTCAGCAGAGATGGACGACGTTTCTGAAGGCTGACCTGC 901
Db 924 ATATGGGGGCGCAGCGGACCTGCAGAGAGAGTGGACACCTTCTCTGAAGCGCGGCTGG 983
QY 902 TGTGCCAGAGGCCGAGCATGGCCGGGCTCCGGGGTCTCGAGGCTATGCGAGAGTTC 961
Db 984 CATGCTCTGCCCCGAACCTGGCAGCTCTACTTCAACCACTGCAGGCGATG---CACACC 1040
QY 962 GGCCTCAGCCTGGAGCGGAACCCCATCTTTTATGGGATCTTTCTCCAGTGGGAAG 1021
Db 1041 TGCAGGACACCTCTGGCAGACACACCACTTCTTTGGGGTTTTCAAGCACAGTGGGTG 1100
QY 1022 GAGCTGCCATCTCTGTGTGCTTCCGACCCCAAGACATCCGGGCGAGTGTGTAATG 1081
Db 1101 ACATGTACTCTGCGGCCATCTGTGAGTACCAGTTTGAAGAGATCCAGCGGTGTTGAGG 1160
QY 1082 GTCCCTTTAGAGAGTAAACATGACTGCACAGGGGACTGCGTGTCAATGACACAGG 1141
Db 1161 GCCCTATTAAGAGTACCATGAGGAAGCCCAAGTGGGACCGCTACACACTGACCCCT---G 1217
QY 1142 TGCCCCAGCCAGACGTGAGAGTGCATCGCCCAACATGAGCTCCAGCAGTTGGAT 1201
Db 1218 TACCAGCCCTCGGCGCTGGCTGCTGCTATTAACACTGGCATCGGCGCCACGGCTACACA 1277
QY 1202 COTCACTCTCCCTGCAGACCGGCTGCTACCTTATCAGAGACCAACCTCTCATGGACA 1261
Db 1278 GCTCCCTGGAGTACCCGACAACTCCTCAACTTGTGTCGAAGAGCACCCGCTGATGGAGG 1337
QY 1262 GCGCGCTTCCCGCTCAGCGCGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1321
Db 1338 AGCAGTGGGCGCTCGGTGGAGCGCGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1397
QY 1322 GAGTCTGCTGCGCACAGGCTGACAGCCCTCTCAGGGAAGAATATGACGTGCTCTACCTGG 1381
Db 1398 ACCTGGTGGCGACCGGTTACAGGACTGTGAGGCCACCTATACAGTGTCTGTTCAATG 1457
QY 1382 GGACAGAGATGGACACCTCCACCGGGTGTGCGCATTTGGAGCTCAGCTCAGTGTCTTGG 1441
Db 1458 GCACAGGAGCGGCTGGCTGCTCAAGGCTGTGAGCGCTGGGCGCTTCCACCTGATTG 1517
QY 1442 AGGATCTGGCTTGT---CCAGNACACAGCCGGTTGAGAGCATGAATTTGACACAG 1498
Db 1518 AGGAGCTCAGCTGTTTGACAGGAGGCCCATGAGAAGCCTGTGCTATCTCAGAGCAAGA 1577
QY 1499 ATTGGCTCTGTGGGCTCCCATCTAGGTGACACAAGTGAACACCAAGCACTGTGGCC 1558
Db 1578 AGCTGCTCTTTGCGGCTCCCGCTCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1637
QY 1559 GTCCTCAGAGTGTGCGAGTGTATCTTGGCCCGAGCCCGGTGTGCGCCTTGGAGCTTCC 1618
Db 1638 AGTATCGCTCTGTGCAGACTGTGCTTCCGCGCGGACCCCTATTGCGCCTTGGAGCGTCA 1697
QY 1619 GCCTTGATGCTGTGTGCGCCACAGCCGCGGA 1649
Db 1698 ACACAGCCGCTGTGTGCGCGTGGGTGCCCA 1728

RESULT 15
AAC84887

AC84887 standard; cDNA; 2155 BP.
AAC84887;
20-APR-2001 (first entry)
Human SEC6 nucleic acid sequence (clone ID 20422974.0.132).
SEC6; cytostatic; gynecological; gene therapy; screening assay; human;
chromosomal mapping; forensic biology; cell proliferation; cancer;
cell differentiation; immune associated disorder; gestational disease;
SEC6; ss.
Homo sapiens.
Key Location/Qualifiers
CD5 166..1937
/*tag= a
/product= "SEC6"
WO200078802-A2.
28-DEC-2000.
23-JUN-2000; 2000WO-US17328.
23-JUN-1999; 99US-0140584.
20-JUL-1999; 99US-0144722.
16-SEP-1999; 99US-0154520.
22-JUN-2000; 2000US-0604286.
(CURA-) CURAGEN CORP.
Shmkets RA, Fernandes E, Vernet C, Yang M, Boldog FL;
Herrmann JL;
WPI; 2001-071385/08.
P-PSDB; AAB48373.
Polynucleotides encoding SECX proteins useful for treating disease
characterized by an aberrant level of cell proliferation and/or
differentiation like cancer or immune associated disorders -
Claim 3; Fig 6; 132pp; English.
The invention relates to human SECX polypeptides and polynucleotides
encoding them. The SECX polypeptides can be expressed by standard
recombinant methodology. The SECX polypeptides are useful for treating
or preventing a SECX-associated disorder. The invention is useful in
screening assays; detection assays (e.g. chromosomal mapping, cell and
tissue typing, forensic biology); predictive medicine (diagnostic assays,
prognostic assays, monitoring clinical trials, and pharmacogenomics); and
methods of treatment (e.g. therapeutic and prophylactic), especially
disorders characterized by aberrant cell proliferation and/or
differentiation like cancer or immune associated disorders or gestational
disease. The present sequence represents a SEC6 nucleic acid sequence.
Sequence 2155 BP; 444 A; 614 C; 645 G; 452 T; 0 other;
Query Match 10.7%; Score 248.6; DB 22; Length 2155;
Best Local Similarity 52.1%; Pred. No. 1.3e-53;
Matches 704; Conservative 0; Mismatches 629; Indels 18; Gaps 6;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 2, Appli
Sequence 2, Appli
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Sequence 1, Appli


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; APPLICANT: KIMURA, Kaoru
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN W
; FILE REFERENCE: 20-456P
; CURRENT APPLICATION NUMBER: US/09/284,180
; CURRENT FILING DATE: 1999-06-09
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; SOFTWARE: PatentIn Ver. 2.0
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; FEATURE:
; OTHER INFORMATION: Coding region from residue 76 to 2406
; NAME/KEY: 3'UTR
; LOCATION: ( )..(3977)
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FEATURE:
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LOCATION: (4008)
US-09-284-180-1

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Table with 10 columns: QY, Db, QY, Db, QY, Db, QY, Db, QY, Db. Rows contain sequence alignment data with various symbols like asterisks, dots, and dashes.

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QY 1498 GATTTGCTCTGTGGGCTCCCATATCAGGTGACACAAAGTGAACACCAAGCACTGTGGC 1557
Db 1501 GATTTGCTCTGTGGGCTCCCATATCAGGTGACACAAAGTGAACACCAAGCACTGTGGC 1560
QY 1558 CGTCTCCAGAGCTGCTCGAGTGTATCTTGGCCCGACGACCCCGTGTGCCCTGGAGCTTC 1617
Db 1561 CGTCTCCAGAGCTGCTCAGAAATGTATCTTGGCCCGACGATCCGCTGTGTGCCCTGGAGCTTC 1620
QY 1618 CGGCTTGATGCTGTGTGGCCACAGCGCGGAGCAGCGGGATGTTTCAAGATATAGAG 1677
Db 1621 CGGCTCGATGCTGTGTGGCCCATCGAGCGGAGCACCCTGGGATGTTTCAAGACATAGAG 1680
QY 1678 TCAGCGGATGTCTCTTCTTTGTGTCCAAAGAACCTTGGAGAACATCCCGTAGTGTGAA 1737
Db 1681 TCAGCAGATGTCTCTTCTTTGTGTCCAAAGAACCTTGGAGAACATCCCGTAGTGTGAA 1740
QY 1738 GTTCCGGTGGCTACTGTGGCCACAGTGTGCTTCCCATGTTTCCCGAGTCTGCCCTGGGGA 1797
Db 1741 GTTCCAGTGGCTACGGTGGGCCACAGTGTGCTTCCCATGTTTCCCGAGTCTGCCCTGGGGA 1800
QY 1798 TCTGTGTGTGGCACCAGCCAGTGGAGTGAAGTGCCTCACCTCCCGAGGATGAGCTA 1857
Db 1801 TCTGTGTGTGGCACCAGCCAGTGGAGTGAAGTGCCTCACCTCCCGAGGATGGGCTA 1860
QY 1858 GAGGTGGTGTGACCCAGGGGCCATGGGGCTTATGCTTGGAGTGTGAGGAGGTGGA 1917
Db 1861 GAGGTGGTGTGACCCAGGGGCCATGGGGCTTATGCTTGGAGTGTGAGGAGGTGGA 1920
QY 1918 GCCGCCCGGTGGTGGCTTATAGCTTGTGTGGGACGCCAGCGGGACCCCTCAAAC 1977

Db 1921 GCGGCCGCTGTGTGGCTGCTTTATAGCTTGGTGTGGGCGACGAGGGGGCCCGCAAC 1980
QY 1978 CCGGCCACACCGTTGTGTGGGCTGATGTTGGCTTCTCTGGGTGTTCTTTCAGCA 2037
Db 1981 CCGGCCACACCGTTGTGTGGGCTGATGTTGGCTTCTCTGGGTGTTCTTTCAGCA 2040
QY 2038 TCCCTCACCTCTCTCTCTGATTTGCTGCCCTCAGCAGCGTCCGCGACAGAGGAGCTTCTA 2097
Db 2041 TCTCTCACCTCTCTCTCTGATTTGCTGCCCTCAGCAGCGGCGGACAGAGGAGCTTCTA 2100
QY 2098 GCTAGAGACAAGTGGGCTTAGATCTGGGGCTTCCACCTTCTTGGGACCAAGCTATAGT 2157
Db 2101 GCTAGAGACAAGTGGGCTTAGATCTGGGGCTTCCACCTTCTTGGGACCAAGCTATAGC 2160
QY 2158 CAGGACCTCTCTCTCTGCTGAGATGAACGCTGCCCTGCCCTGGGTAAAGCGG 2217
Db 2161 CAGGACCTCTCTCTCTGCTGAGATGAACGCTGCCCTGGGCTAAAGCGG 2220
QY 2218 GGCAGTGGTTTGGTGGCTTCCCTCCACCTTCTCTGCTGATTTTGGCCAAAGCCAGCC 2277
Db 2221 GGCAGTGGTTTGGTGGCTTCCCTCCACCTTCTCTGCTGATTTTGGCCAGCCAGCC 2280
QY 2278 CACATCCGCTCAGTGGGGGCTCTAGCCAGCTGTGATGAGACCTTCCATCTAA 2331
Db 2281 CACATCCGCTCAGTGGGGCTCTCTGGCCACGTGCGATGAGACGCTTATCTAA 2334

RESULT 6
US-60-360-207-19015
; Sequence 19015, Application US/60360207
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: C1001321
; CURRENT APPLICATION NUMBER: US/60/360, 207
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 19015
; LENGTH: 2334
; TYPE: DNA
; ORGANISM: HUMAN
US-60-360-207-19015

Query Match 91.8%; Score 2138.8; DB 91; Length 2334;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 2219; Conservative 0; Mismatches 112; Indels 3; Gaps 1;

QY 1 ATGCTTGGCAGGGCGAGGGCCCGCCCGGGCGCCCGCGGCTCTTTCCTTC 60
Db 1 ATGCTGGCCAGGGCGAGGGCCCGCCCGGGCGCCCGCGGCTCTCTCTTC 60
QY 61 CCGCGCGCGCTCTC--GCTGCTGCTGCTGCTGGGATGCTGAGCGCCGGGTGCGGC 117
Db 61 CCGCGCGCGCTCTCCTGCTGCTGCTGCTGGGATGCTGAGCGCCGGGTGCGGC 120
QY 118 CCGCTCCCGCTCAGTGGCCAGAACCTCGCTGCCCATCTCCGAGGCTGACTCTATCTC 177
Db 121 CCGCTCCCGCTCAGTGGCCAGAACCTCGCTGCCCATCTCCGAGGCTGACTCTATCTC 180
QY 178 ACCCGGTTTGGAGCTCTCATACGATACATTTACTCTGCTCTCTTGTGATCCTGCTCC 237
Db 181 ACCCGGTTTGGCGCCCTCATACGATACATTTACTCTGCTCTCTTGTGATCCTGCTCT 240
QY 238 CACACACTTACGTCGGTGCAGGGATAGCATTTTGGTTTAAACCTCCCTTCCTCTGG 297
Db 241 CACACACTTACGTCGGTGCAGGGATAGCATTTTGGTTTAAACCTTCCTCTCTGG 300
QY 298 GAAAGACCCGAAAGGATCGACTGGATGGTACCTGAGACTCACAGACAGAACTGCAGGA 357
Db 301 GAAAGACCTCGAAGATCGACTGGATGGTGGCCGAGACTCACAGACAGAACTGTAGGA 360
QY 358 AAAGGCAAGAAAGAGGAGAAATGTCAAAATTTTATCCAGATTTCTGCCATTTGCAATGCC 417

Db 361 AAAGCAAGAAAGAGGACGAATGTACAAATTTATCCAGATTTCTCGCCATTTGCCAATGCC 420
Qy 418 TCTCACCTCTCAGTCGGGACCTTCGCTTTTGTATCCGAGTGCAGGCTATGATGTG 477
Db 421 TCTCACCTCTCAGTCGGGACCTTCGCTTTTGTATCCGAGTGCAGGCTATGATGTG 480
Qy 478 TCCAGTTTCCAGCAGGTTGAAGACTTGAAGCGCCGGGGGAAATGCTTTTGAAGCCA 537
Db 481 TCCAGTTTCCAGCAGGTTGAAGACTTGAAGTGCAGGCGGGAATGCTTTTGAAGCCA 540
Qy 538 GCTCAAGCGTCAGCAGCTGAATGGCTGGGGGCTCTCTACACCGCCACTGTGAAGAAC 597
Db 541 GCTCAAGCGTCAGCAGCTGAATGGCTGGGGGCTCTCTACACCGCCACTGTGAAGAAC 600
Qy 598 TTCTGTGGGACTGAGCCCATCATCTCCGAGCTGTGGTGCAGCTGAGGACTGATTCGA 657
Db 601 TTCTGTGGGACTGAGCCCATCATCTCCGAGCTGTGGTGCAGCTGAGGACTGATTCGA 660
Qy 658 ACAGAGACCTTGTCTATCTGTGCTTAATGCTCCAGCCTTTGTGCGAGCTATGGTCTGAGC 717
Db 661 ACAGAGACCTTGTCTATCTGTGCTTAATGCTCCAGCCTTTGTGCGAGCTATGGTCTGAGC 720
Qy 718 CCAGCTGAGTGGGGGATGAAGATGGAGACGATGAAATCTTTTTCCTCACGGAGACC 777
Db 721 CCGCTGAGTGGGGGATGAAGATGGAGACGATGAAATCTTTTTCCTCACGGAGACC 780
Qy 778 TCCGAGCTGTGGGACTCTATGAGCGCATCAAGTCCCAAGAGTGCAGGCTGTGGCG 837
Db 781 TCCGAGCTGTGGGACTCTATGAGCGCATCAAGTCCCAAGAGTGCAGGCTGTGGCG 840
Qy 838 GGGGACCTTGGGGGAGAGACCTTTCAGCAGAGATGGAGACGTTTCTGAAGGCTGAC 897
Db 841 GGGGACCTTGGGGGAGAGACCTTTCAGCAGAGATGGAGACGTTTCTGAAGGCTGAC 900
Qy 898 CTGCTGTGCCAGGGCCGAGCATGGCCGGGCTTCGGGGTTCGAGGCTTGGGACAG 957
Db 901 CTGCTGTGTCCAGGGCCGAGCATGGAAGGGGCTTCGGGGTTCGAGGATATGACAGAG 960
Qy 958 CTTCGGCTCAGCTGTGGAGGGGAAACCCCATCTTTTATGGGATCTTTCTCCAGTGG 1017
Db 961 CTTCGACCTCAGCTGTGGGGGAGACCCCTCTTTTATGGCATCTTTCTCCAGTGG 1020
Qy 1018 GAAGAGCTGCCATCTCTGTGTGTGTGCTTCCGACCCCAAGACATCCGGGAGTGTG 1077
Db 1021 GAAGGAGCGGCAATTTCTGTGTGTGTGCTTCCGACCCCAAGACATCCGGGAGTGTG 1080
Qy 1078 AATGGTCCCTTTAGAGACTAAACATGACTGCAACAGGGGACTGCCTGTCTATGGACAAC 1137
Db 1081 AATGGTCCCTTTAGAGACTAAACATGACTGCAACAGGGGACTGCCTGTCTATGGACAAC 1140
Qy 1138 GAGTGTCCCAAGCCAGACCTGGAGAGTGCATCGCAACACATGAAGCTCCAGCAGTTT 1197
Db 1141 GAGTGTCCCAAGCCAGACCTGGAGAGTGCATCGCAACACATGAAGTCCAGCAGTTT 1200
Qy 1198 GGATCTCTACTCTCCCTGCCAGACCGGTGTCTACCTTTATCAGAGACCAACCTCTCATG 1257
Db 1201 GGATCTCTACTCTCCCTGCCAGACCGGTGTCTACCTTTATCAGAGACCAACCTCTCATG 1260
Qy 1258 GACAGGCGGTGTCCGGCTGAGCGGCGGCCCCCTGTGGTCACTACAGATACAGCCTAT 1317
Db 1261 GACAGGCGGTGTGTCCAGCTGATGGCGGCCCCCTGTGGTCACTACAGATACAGCCTAT 1320
Qy 1318 CTCAGAGTCGTGGCCCAAGGCTGACAGGCTCTCAGGGAAGAATATGAGTCTCTAC 1377
Db 1321 CTCAGAGTCGTGGCTACCGGGTACCCAGCTCTCAGGGAAGAATATGAGTCTCTAC 1380
Qy 1378 CTGGGACAGAGGATGGACACTCCACCGGCTGTGGCATTTGGAGCTCAGCTCAGTGTG 1437
Db 1381 CTGGGACAGAGGATGGGACCTCTCATCGGGCTGTGGCATCGGAGCTCAGCTCAGTGTG 1440
Qy 1438 TTGAGGATCTGGGCTGTGTCCTCCAGACCAACCGGTTGAGAGCATGAAATTTGATACCAG 1497
|||||

Db 1441 CTGSAGGATCGGCTTTGTTCCGGAACACAGCCGTTGAAAGCATGAAATTTGATACCAT 1500
Qy 1498 GATTGGCTCTGTGGTGGCTCCCATACTAGTGACAAAGTGACACAGCACTGTGGC 1557
Db 1501 GATTGGCTCTGTGGTGGCTCCCATACTAGTGACAAAGTGACACAGCACTGTGGC 1560
Qy 1558 CGTCTCCAGAGCTGCTCGGAGTATCTTGGCCAGAGCCCGTGTGGGCTGTGAGGCTTC 1617
Db 1561 CGTCTCCAGAGCTGCTCAGAATGTATCTGCGCCAGGATCCCGTGTGCTGTGAGGCTTC 1620
Qy 1618 CGGCTTATGATGCTGTGTGGCCAGCGCGGAGCACCGCGGATGGTTCAAGATATAGAG 1677
Db 1621 CGGCTTATGATGCTGTGTGGCCATGAGCGGAGCACCGTGGATGGTTCAAGATATAGAG 1680
Qy 1678 TCAGCGATGCTCTCTTTGTGTCAAAGAACTGGAAGAACTCCCGTAGTGTGAA 1737
Db 1681 TCAGCGATGCTCTCTTTGTGTCAAAGAACTGGAAGAACTCCCGTAGTGTGAA 1740
Qy 1738 GTTCCGCTGCTACTGTGGGCCAGTGTCTGCTGCTATGTTCCCGCAGTGTGCTGTGGCA 1797
Db 1741 GTTCCAGTGGCTACGTTGGGCCAGTGTCTGCTGCTATGTTCCCGCAGTGTGCTGTGGCA 1800
Qy 1798 TCCTGTGTGGCACAGCCAGTGGAGTACTGCTGCTACTCCCCGAGGATGGACTA 1857
Db 1801 TCCTGTGTGGCACAGCCAGTGGAGTACTGCTGCTACTCCCCGAGGATGGGCTA 1860
Qy 1858 GAGTGTGTGTGACCCAGGGCCATGGGGCTTATGTTGCGAGTGTGAGAGGGTGA 1917
Db 1861 GAGTGTGTGTGACCCAGGGCCATGGGGCTTATGTTGCGAGTGTGAGAGGGTGA 1920
Qy 1918 GCGCCCGCTGTGTGGCTTATAGTGTGTGGGCGAGCCAGCGGGGACCTCAAAAC 1977
Db 1921 GCGCCCGCTGTGTGGCTTATAGTGTGTGGGCGAGCCAGCGGGGCGCCGCAAAAC 1980
Qy 1978 CGGCCCCACACCTGTGTGGGCTGAGTGGTTGGCTTTCTCTGCGTGTGTTGCGAGCA 2037
Db 1981 CGGCCCCACACCTGTGTGGGCTGAGTGGTTGGCTTTCTCTGCGTGTGTTGCGAGCA 2040
Qy 2038 TCCCTCACTCTCCCTCTGATTGTGCGCGTCAGCAGCGTGTGGGCGAGAGGAGCTTCTA 2097
Db 2041 TCTCTCACTCTCCCTCTGATTGTGCGCGTCAGCAGCGGCGGCGAGAGGAGCTTCTA 2100
Qy 2098 GCTAGACAAAGTGGGCTTAGATCTGGGGCTCCACCTTCTTGGGACACAAAGCTATAGT 2157
Db 2101 GCTAGACAAAGTGGGCTTAGATCTGGGGCTCCACCTTCTTGGGACACAAAGCTATAGC 2160
Qy 2158 CAGGACCTCCCTCTCTCTGTGCGCTGAAGTGAACGCTGCGGCTGGGCTGGGTAAAGCGG 2217
Db 2161 CAAGACCTCCCTCTCTCTTACCTGAAGTGAACGCTGCGGCTGGGCTGGGTAAAGCGG 2220
Qy 2218 GGCAGTGTGTTGTTGGCTTCCCTCCACCTTCTCTGCTGATTTGCCCCAAGCCCCAGCC 2277
Db 2221 GGCAGTGTGTTGTTGGCTTCCCTCCACCTTCTCTGCTGATTTGCCCCGAGCCCCAGCC 2280
Qy 2278 CACATCGGCTCACTGGGGGCGCTCTAGCCAGTGTGATGAGACCTTCATCTAA 2331
Db 2281 CACATCGGCTCACTGGGGGCTCTCTGCGCCACGTCGATGAGAGCTTATCTAA 2334
|||||

RESULT 7

US-09-611-523-65

; Sequence 65, Application us/09611523

; GENERAL INFORMATION:

; APPLICANT: OTA, TOSHIO

; APPLICANT: ISOGAI, TAKAO

; APPLICANT: NISHIKAWA, TETSUO

; APPLICANT: KAWAI, YURI

; APPLICANT: SUGIYAMA, TOMOYASU

; APPLICANT: HAYASHI, KOJI

; TITLE OF INVENTION: SECRETORY PROTEIN OR MEMBRANE PROTEIN

; FILE REFERENCE: 08435/0121

; CURRENT APPLICATION NUMBER: US/09/611,523

; CURRENT FILING DATE: 2000-07-07

1888 TGTGTGTGGCACCACCCAGTGGAGTGACTGCACCTACCCCCCGCGGGATGGAGTGGAG 1947
1861 GTGGTGGTGAACCCAGGGCCATGGGCTTATGCTTGCAGTGTTCAGAGGGTGGAGCC 1920
1948 GTGGTGGTGAACCCAGGGCCATGGGCTTATGCTTGTGAATGTCAAGAGGGTGGGCA 2007
1921 GCCCGCGTGGTGGCTTATAGCTTGGTGGGCGAGCCAGCGGGGACCTTCAAAACGG 1980
2008 GCCCATGTGGTAGCAGCTTACAGCTTGGTATGGGCGAGCCAGCGAGAGTCTCCGAGCCG 2067
1981 GCCCACACGGTGTGGGGGCTGGATGGTGGCTTTCCTGGGTGGTTCCTGCAGCATCC 2040
2068 GCCCACAC---AGTGGGGGCGGAGCTGGCTGGCTTCTTGGGGATTCTCGCAGCATCC 2124
2041 CTCACCTCTCCTCTGATTGGTGGCGCTCAGCAGCGTGGCGGACAGGAGGAGCTTCTAGCT 2100
2125 CTGACTCTCATCTGATTGGTGGCGCTCAGCAGCGGCGGACAGGCGGACAGGGAAGTCTGGCT 2184
2101 AGAGACAAGTGGGCTTATAGTCTGGGGCTCCACCTTCTGGGACACAAAGCTATAGTCAG 2160
2185 AGAGACAAGTGGGCTGGACCTGGGGGCTCCACCTTCTGGGACACAAAGCTTACAGCCAA 2244
2161 GACCTCTCCTCTCCTCTGCGCTGAAGTGAACGGCTGGCCCTGGGTAAGCGGGC 2220
2245 GACCTCTCCTCTCCTCTGCGCTGAAGTGAACGGCTGGCCCTGGGTAAGCGGGC 2304
2221 AGTGGTGGTGGCTTCCCTCCACCTTCTGCTGGATTCTTGCCCAAGCCAGCCAC 2280
2305 AGTGGCTGGTGGATTCTCACCACCTTCTGCTGGATTCTTGCCCAAGCCAGCCAC 2364
2281 APTCCGGCTCACTGGGGCGCTCTAGCCAGCTGTGATGAGACCTCCACTA 2330
2365 ATTCCGGCTAACTGGGGCTCTCTAGCCACATGTGATGAACATCCACTA 2414

RESULT 8

US-10-305-278-65
; Sequence 65, Application US/10305278
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: KAWAI, YURI
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: HAYASHI, KOJI
; TITLE OF INVENTION: SECRETORY PROTEIN OR MEMBRANE PROTEIN
; FILE REFERENCE: 084335/0121
; CURRENT APPLICATION NUMBER: US/10/305,278
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: US/09/611,523
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: JP 1999-194179
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: JP 2000-118775
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183766
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/159,586
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 60/183,323
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 679
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 2971
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (103)..(2412)
US-10-305-278-65

Query Match 78.4%; Score 1827.6; DB 50; Length 2971;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 2033; Conservative 0; Mismatches 279; Indels 18; Gaps 2;
QY 1 ATGCTTGGCAGGGCCGAGGGCCCGCGCGGGCCCGCGGGCCCGCGGGCTCCGGTCTTTCCTTC 60
DB 103 ATGCGGGCTCTGCTGCGCGCGCGCGCGGGTCCCGGCGAGCTTACAGCTTCGCGCTTC 162
QY 61 CGCGCGCGCGCTGCTGCTGCTGCTGGGCGATTAAGCGCGCGCGGGTGTGGCGCGCG 120
DB 163 CC-----GCTACTGCTGCTGGCGGTGCTGAGCGCGCGGGTATCCGCGCGCG 207
QY 121 GTCCCCCGCTCAGTCCCGCAGAACCTCGCTGCCCATCTCCGAGGCTGACTTCCTATCTCACC 180
DB 208 GTCCCCCGCTCGGTGCCAGAACCTCGCTTCCAATCTCTGAGGCTGACTTCCTGTCTCACC 267
QY 181 CGGTTTGCAGCGCTCTCATACGTACAAATTAATCTGCTGCTCTCTGCTGATGATGCTCCCT 240
DB 268 CGGTTTGCAGCGCTCTCACACATACAAATTAATCTGCTGCTCTCTGCTGATGCTCCCTCCAC 327
QY 241 ACACCTTTACGTCGGTGCACGGGATAGCATCTTTCGCTTTAAACCTTCCCTTCTCTGGGAA 300
DB 328 ACACCTTTATGTGGCGCGCGGACACCATCTTCGCTTTATCCCTGCCCTTCTCAGGGAG 387
QY 301 AGACCCCGAAGGATCGACTGGATGATCTGAGATCTACAGACAGAACTGCAAGAGAAA 360
DB 388 AGACCCCGCAGGATTTGACTGGATGTTCTCTGAGGCTCACAGACAGAACTGTAGGAAGAAA 447
QY 361 GCGAAGAAGAGGAGCAATGTACAAATTTTATCCAGATTCGCCCATGTGCAATGCCCTCT 420
DB 448 GCGAAGAAGAGGAGCAATGTACAAATTTTGTCCAGATTTCTGCCCATGTGCCAATGCCCTCT 507
QY 421 CACCTCTCACGTGCGGACCTTTCGCTTTTGTATCCGAAGTGGGGGTATTGATGTGTC 480
DB 508 CACCTCTCACGTGCGGACCTTTCGCTTTTGTATCCGAAGTGGGGGTATTGATGTGTC 567
QY 481 AGTTCCAGCAGGTTGAAAGACTTGAGAGCGCGCGGGGAAATGCTCTTTTGAGCCAGCT 540
DB 568 AGTTCCAGCAGGTTGAAAGACTTGAGAGTGGCGGGGAAATGCTCTTTTGAGCCAGCT 627
QY 541 CAACGGTCAGCAGCTGTAATGCTGGGGCGTCTCTACACCGCCACTGTGAAGAACTTC 600
DB 628 CAGCGGTGAGCAGCTGTAATGCTGGGGCGTCTCTATGCTGCCCATGTGAAAACTAC 687
QY 601 CTGGGGACTGAGCCCATCATCTCCGAGCTGTGGGTCCGAGCTGAGGACTGGATTCGAACA 660
DB 688 CTGGGGACGAGCCCAATTAATCACAGACAGTGGGTGCTGCGCGAGGAGTGGATTCGACA 747
QY 661 GAGACCTTGTATCTCTGCTTAATGCTCCAGCTTTTGTGCGAGCTATGGTCTCTGAGCCCA 720
DB 748 GATACCTTGCTTCTGCTGCTGAACCGCCGAGCTTTGTGCGAGCGCTGGCTTGAGCCCA 807
QY 721 GCTGAGTGGGGGATGAAGATCGACAGTGAATGAAATCTTTTCTTCTTACGAGAGCTTC 780
DB 808 GCCGAATGGGGGATGAAGATGGAGACGACGAATCTACTTCTTCTTACGAGAGACTTC 867
QY 781 CGAGTGTGTGACTCTCTATGAGCGCATCAAGGTGCCAAGAGTGGCGCGAGTGTGCGGG 840
DB 868 CGAGCATTTGACTCATACAGCGCATTAAGTCCACGCGGTGGCGCGGTGTGTGCGGG 927
QY 841 GACCTTGGGGGAGGAAGACCTTTCAGCAGAGATGGAGACATTTTCTTGAAGCTGACCTG 900
DB 928 GACCTCGGGGGCGGAAGACCTTCCAGCAGAGATGAGCAGCTTTTGAAGCTGACCTG 987
QY 901 CTGTGCCAGGGCCCGAGCATGGCGGGCTCCGGGGTCTCGAGGCTATGCGAGGCTT 960
DB 988 CTCTGTCCAGGCGCTGAGCATGGCGGGCTCCAGTGTCTCTCAGAGATGTTCTGTGCTT 1047
QY 961 CGGCTCTCAGCTGAGCGGGAACCCCATCTTTTATGGATCTTTTCTCCAGTGGGAA 1020
DB 1048 CGACCTGAGCTTGGGGCAGGGACTCCCATCTTTTATGGCATCTTTTCTCCAGTGGGAG 1107
QY 1021 GGAGCTGCCATCTCTGCTGTGTGCTTCCGACCCCAAGACATCCGGGCGAGTGTGTAAT 1080

Db 1108 GGGGCTACTATCTCTGTGCTGTGCTTCCGACCACAAGACATTCGGACAGTGCTGAAT 1167
Qy 1081 GGTCCCTTTAGAGAGCTAAACATGACTGCAACAGGGGACTGCTGTCTATGGACAACGAG 1140
Db 1168 GGTCCCTTCAGAACTAAACATGACTGCAACAGAGGACTGCTGTCTGGACAATGAT 1227
Qy 1141 GTGCCCCAGCCAGACTGGAGAGTGCATGCGCAACAACATGAAGTCCAGCAGTTTGGGA 1200
Db 1228 GTGCCCCAGCCAGACTGGAGAGTGCATCAACCAACAACATGAAGTCCGCGCACTTTGGC 1287
Qy 1201 TCCCTCACTCTCCCTGCCAGACCCGGTGTCTACCTTTATCAGACACACCTCTCATGGAC 1260
Db 1288 TCATCTCTCTCCCTGTGCTGACCCGCTACTCACCTTCATCGGAGACCACCACTCATGGAC 1347
Qy 1261 AGCCCGCTGTTCCTCCGCTGACGCGCCCTGCTGTCTCACTACAGATACAGCTATCTC 1320
Db 1348 AGCCAGTGTTCACAGTGTATGCCACCCCTGCTGTCACTACAGATACAGCTATCTC 1407
Qy 1321 AGAGTCGTGGCCACACAGGTGACAGCCTCTCAGGAAAGAAATATGACGTGTCTACCTG 1380
Db 1408 AGAGTCGTGGCCACACAGGTGACAGCCTCTCAGGAAAGAGTATGATGTGCTCTACCTG 1467
Qy 1381 GGCACAGAGATGGACACCTCCACCGGCTGTCGCAATTGGAGCTCAGCTCAGCTGCTTG 1440
Db 1468 GGCACAGAGATGGACACCTCCACCGAGCAGTCCGATCGGAGCTCAGCTCAGCTGCTTT 1527
Qy 1441 GAGGATCTGGCCTTGTTCACAGAACACAGCCGTTGAGAGCATGAATTTGACACAGAT 1500
Db 1528 GAAGATCTGGCCTTATCCAGAGACACAGCCAGTTGAGACATGAATTTGACACAGC 1587
Qy 1501 TGGCTCCTGTGGGCTCCCATACTGAGGTGACAAAGTGACAAAGTGAACACCACTGTGCCGT 1560
Db 1588 TGGCTCCTGTGGTCCCGTACTGAGGTGACAAAGTGAATTAACAACCACTGTGCCGT 1647
Qy 1561 CTCACAGCTGCTCGAGTGTATCTTGGCCAGGACCCCGTGTGCGCTGGAGCTTCGG 1620
Db 1648 CTCACAGCTGCTCAGAGTGATCTTGGCCAGGACCCAGTCTGTGCTTGGAGCTTCGG 1707
Qy 1621 CTTGATGCTGTGTGGCCACGCGCGAGCACCGGGATGGTTCAAGATATAGAGTCA 1680
Db 1708 CTGATGAGTGTGTGCCCATGCCGGGAGCACCGAGGGTGGTCCAAACATAGAGTCA 1767
Qy 1681 GCGGATGCTCTCTTTGTGTCAAAGAACCTGGAGAACATCCCGTAGTGTGTTGAAGTT 1740
Db 1768 GCAGATGCTCTCTTTGTGTCCTAAAGAGCCTGGAGAACGTCACGATGTTGAAGTT 1827
Qy 1741 CCGGTGGCTACTGTGGCCACGCTGTCCTGCCATGTTCCCGCAGTCTGCCCTGGCATCC 1800
Db 1828 CCGGTGGCTACAGCTCGCATGTGGTGTGGCATGTTCTCCAAGCTPCAGCATGGGCATCC 1887
Qy 1801 TGTGTGTGACACAGCCCACTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1860
Db 1888 TGTGTGTGACACAGCCCACTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1947
Qy 1861 GTGGTGTGACCCAGGGCCATGGGGGCTTATGCTTGGAGTGTGAGGAGGTGGAGCC 1920
Db 1948 GTGGTGTGACCCAGGGCCATGGGGGCTTATGCTTGAATGTGAGGAGGTGGGGCA 2007
Qy 1921 GCGCGGTGGTGGCTTATAGCTTGTGCTGGGCGACCGGGGACCCCTCAACCCG 1980
Db 2008 GCCATGTGTAGACCTTACAGCTTGGTATGGGCGACCGAGAGATGCTCCGAGCCGG 2067
Qy 1981 GCCACACCGTGTGGGGCTTGAATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2040
Db 2068 GCCACAC - - AGTGGGGGGGAGCTGGCTGGCTTCTTCTGGGATTTCTCGCAGATCC 2124
Qy 2041 CTCACCTCTCTCTGATGGTGGCTCAGCAGCTGCGGACAGAGGAGCTTCTAGCT 2100
Db 2125 CTGACTCTCATTTCTGATGGTGGCTCAGCAGCTGCGGAGCGGAGAGGAACTTCTGGCT 2184
Qy 2101 AGAGACAAGGTGGGCTTAGATCTGGGGGCTCCACCTTCTGGGACCAAGCTATAGTCAG 2160

Db 2185 AGAGACAAGGTGGGCTGGACCTGGGGGCTCCACCTTCTGGGACCACAAGCTACAGCCAA 2244
Qy 2161 GACCCTCCCTCTCTCTTGGCTGAAGATGAACGCTGCCCTGGCTTGGTAAGCGGGC 2220
Db 2245 GACCCTCCCTCCCTCTCTTGAAGATGAGCGTGGCGCTGGCCCTGGCAAGAGGGC 2304
Qy 2221 AGTGGTTTGGTGGCTTCCCTCCACCTTCCCTGCTGATGCTTTCGCAAGCCAGCCAC 2280
Db 2305 AGTGGCTTGGTGATTCACCACTTCTCTGCTTGTGCTTGGCCAGCCAGCCAC 2364
Qy 2281 ATCCGCTCAGTGGGGGCTCTAGCCACGCTGTGATGAGACCTTCCATCTA 2330
Db 2365 ATTCGGCTAACTGGGCTCTCTAGCCACATGATGAACATCCATCTA 2414

RESULT 9
US-10-170-235-32596
; Sequence 32596, Application US/10170235
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HU
; TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
; FILE REFERENCE: CL001380
; CURRENT APPLICATION NUMBER: US/10/170,235
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 32596
; LENGTH: 3641
; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-32596

Query Match 78.4%; Score 1827.6; DB 47; Length 3641;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 2033; Conservative 0; Mismatches 279; Indels 18; Gaps 2;

Qy 1 ATGCTTTGCCAGGCGCAGCGGCGCCCGCGGGCGCCCGCGGCGCTCCGGTCTTTCCTTC 60
Db 87 ATGCGGCGCTCTGCTCGCGGCGCCCGCGGGTCCCGGCGAGCTACAGCGCTCGCGCTTC 146
Qy 61 CGCGCGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 147 CC-----GCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 191
Qy 121 GTCCCGCGCTCAGTGGCCAGAACCTCGCTGCCCATCTCGAGGCTGACTCTCTATCTCACC 180
Db 192 GTCCCGCGCTCGGTGCCAGAACCTCGCTTCCAATCTCTGAGGCTGACTCTCTCTCACC 251
Qy 181 CGGTTTGCAGGCTCATACGTACAATTTACTCTGCTCTCTCTGTTGGATCTGCTCTCCAC 240
Db 252 CGGTTTGCAGTCTCTCACACATACAATTTACTCTGTTCTCTCTGTTGGATCTGCTCTCC 311
Qy 241 ACATTTTACGTGCGTGCAGGGATAGCATCTTTCGCTTTTAAACCTTCCCTTCTCTGGGAA 300
Db 312 ACATTTTATGTTGGCGCCCGGACACCATCTTTCGCTTTTATCCCTGCTCTCTCAGGGAG 371
Qy 301 AGACCCCGAAGGATCGACTGGATGTTACCTGAGACTCACAGACAGAACTGCAGAAAGAA 360
Db 372 AGACCCCGCAGGATTGACTGGATGTTCTGAGGCTCACAGACAGAACTGTAGAAAGAA 431
Qy 361 GCGAAGAAAGAGACCAATGTCAATTTTATCCAGATTTCTGCCATTTGTCAATGCTCT 420
Db 432 GCGAAGAAAGAGACCAATGTCAATTTTGTCCAGATTTCTGCCATTTGCCATTTGCTCT 491
Qy 421 CACCTCTCACGTGCGGCGACCTTTCGCTTTTGTATCCCAAGTGGGGGTTTATGATGTGTC 480
Db 492 CACCTCTCACGTGCGGCGACCTTTCGCTTTTGTATCCCAAGTGGGGGTTTATGATGTGTC 551
Qy 481 AGTTTCCAGAGTTGAAAGACTTGAGACGCGCGCGGGGAAATGTCTTTTGTAGCCAGCT 540
Db 552 AGTTTCCAGAGTTGAAAGACTTGAGAGTGGCGGGGAAATGTCTTTTGTAGCCAGCT 611
Qy 541 CAAAGGTGACAGCTGTAATGCTGGGGGCTCTCTACACCCCACTGTGAAGAACTTC 600

APPLICATION NUMBER: EP 98300693.3
 FILING DATE: 30-JAN-1998
 APPLICATION NUMBER: US 9816423.9
 FILING DATE: 28-JUL-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Prestia, Paul F
 REGISTRATION NUMBER: 23,031
 REFERENCE/DOCKET NUMBER: GP-30036
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 601-407-0700
 TELEFAX: 610-407-0701
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2893 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 US-09-160-762-1

Query Match	69.8%	Score 1626;	DB 16;	Length 2893;
Best Local Similarity	83.2%	Pred. NO. 0;		
Matches 1938;	Conservative	0;	Mismatches 275;	Indels 117;
				Gaps 3

Qy	1	ATGCTTGCCAGGGCCGACGGCCCGCCGGGCCCCGGCCGCTTCGGGTCTTTCCCTTC	60
Db	110	ATGCGGGCTCTGCTGGCGGCCCGCCGGGTCCCGGGCAGCCTACAGCCTCGGCCCTTC	169
Qy	61	CCGGCCGGCTGTGCTGCTGCTGCTGCTGGCGATATAAGCGGCCGGGTGTGGCGCGC	120
Db	170	CC-----GCTACTGCTGCTGGCGGTGTGAGCGGCCGGTATCGCGCGCGC	214
Qy	121	GTCCCCCGCTCAGTGCCCGAAGACTCGCTGCCCATCTCCGAGGCTGACTCCTATCTCACC	180
Db	215	GTCCCCCGCTCGGTGCCGGAAGACTCGGTCCAAATCTGTGAGGCTGACTCCTGTCTCACC	274
Qy	181	CGGTTTGCAGCGTCTCATGTACAAATTACTCTGCTCTCCTTTGTGGATCTCGCTCCAC	240
Db	275	CGGTTGCGAGTCCCTCACACATACAATTACTCTGTCTCTCTTGTGGATCCTGCCCTCCAC	334
Qy	241	ACACTTACGTCGCTGCACGGGATAGCATCTTTCGTTTAAAGCTCCCTTCTCTGGGAA	300
Db	335	ACACTTATGTTGGCGCCGGGACCATCTTTCGCTTATCCCTGCCCTTCTCAGGGGAG	394
Qy	301	AGACCCCGAAGGATCGACTGGATGGTACTCTGAGACTCACACAGAACTGCAGAGAAGA	360
Db	395	AGACCCCGAGGATTGACTGGATGGTTCCTGAGGCTCACACAGAACTGTAGGAAGAA	454
Qy	361	GGCAAGAAAGAGGACGAATGTCACAATTTTATCCAGATTCTCGCCATTGTCAATGCCCT	420
Db	455	GGCAAGAAAGAG-----	466
Qy	421	CACCTCTCAGCTCGGACCTTCGCTTTTGATCCGAAGTCGGGGGTATTATTGATGTGCC	480
Db	467	-----GATGTGTCC	475
Qy	481	AGTTTCCAGAGTTGAAAGACTTGAGAGCGCGCGGGGAAATGTCTCTTTTTCAGCCAGCT	540
Db	476	AGTTCCAGCAGGTTGAAAGACTTGAGAGTGGCCGGGGGAAATGTCTCTTTTTCAGCCAGCT	535
Qy	541	CAACGGTTCAGCAGCTGTAATGGCTGGGGCGCTCTACACCGGCACCTGTCAAGAACATTC	600
Db	536	CAGGGTTCAGCAGCTGTAATGGCTGGGGGTCTCTATGTCGCACATGTGAAAACATPAC	595
Qy	601	CTGGGGACTGAGCCCATCATCTCCGAGCTGTGGGTTCGAGCTGAGGACTGGATTTCGAACA	660
Db	596	CTGGGACGGAGCCAAATTATCACAGAGCAGTGGGTGTGGTCCGAGGACTGGATTTCGGACA	655
Qy	661	GAGACCTTGATCCTCGCTTAATGCTTCAGCCCTTTGTCCAGACTATGGTCCGTGAGCCCA	720
Db	656	GATACCTTGGCTTCTCGCTGAACGCCGCCAGCCTTTGTTCGAGCGGCTGGCTTCGAGCCA	715

Qy	721	GCTGAGTGGGGGATGAAGATGGAGACGATGAATCTTTTTTTCTTCACGGAGACTCC	780
Db	716	CCCCAATGGGGGATGAAGATGGAGACGAGAAATCTTCTCTTTTACGGAGACTCC	775
Qy	781	CGAGTGTGGAGTCTTATGAGCGCATCAAGGTCCCAAGAGTGGCCCGAGTGTGTGCGGG	840
Db	776	CGAGCATTTTACTCATACGAGCGCATTAAGTCCACGGGTGGCCCGTGTGTGTGCGGG	835
Qy	841	GACCTTGGGSCAGAAAGACCTTCACGACAGATGGACGAGTTTCTTGAAGGCTGACCTG	900
Db	836	GACCTCGGGGCGGAAGACCTCCACGACAGATGGACGAGTTTGTGAAGCTGACCTG	895
Qy	901	CTGTGCCAGGGCCGAGCATGCGCGGGCTCCGGGTCTCGAGGCTATGGCAGACTT	960
Db	896	CTCTGTCCAGGGCTGAGCATGGCGGGCTCCAGTGTCTCGAGGATGTTGCTGTGCTT	955
Qy	961	CGGCTCAGCTTGAGCGGGAACCCCATCTTTTATGGGATCTTTTCTCCAGTGGGA	1020
Db	956	CGACTGAGCTTGGGCGAGGACTCCCATCTTTTATGGCATCTTTCTTCCAGTGGGAG	1015
Qy	1021	GGAGTGGCATCTCTGCTGTGTGTGCTTCCGACCCCAAGACATCCGGGCGAGTCTGAAT	1080
Db	1016	GGGCTACTATCTCTGCTGTCTGTGGCTTCGACCACACAGCATTCGGACAGTCTGAAT	1075
Qy	1081	GGTCCCCTTTAAAGAGCTAAACATGACTGCAACAGGGGACTGCTGTCTATGGACAACGAG	1140
Db	1076	GGTCCCCTCAGAAACTTAAACATGACTGCAACAGGAGACTGCTGTCTGGACAATGAT	1135
Qy	1141	GTGCCCCAGCCAGACCTTGAGAGTGCATCGCCAAACAATGAAGTCCAGCAGTTTGGGA	1200
Db	1136	GTGCCCCAGCCAGACCTTGAGAGTGGATCACCAAACAATGAAGTCCGGCAGTTTGGC	1195
Qy	1201	TCCTCACTCTCCCTGGCAGACCGGTGCTCACCTTTATCAGAGCACACCCTCTCATGGAC	1260
Db	1196	TCATCTCTCTCCCTGCTGACCGGTACTCACCTTATCCGGGACACCACCTCATGGAC	1255
Qy	1261	AGGCCCGTGTCCCGGCTGACGGCGGCCCTCTGCTGTCTACTACAGATACAGCCTATCTC	1320
Db	1256	AGGCCAGTGTTCAGCTGATGGCCACCCCTCTGCTGTCTACTACAGATACAGCCTATCTC	1315
Qy	1321	AGAGTCGTGGCCACAGGSGTACCAGCTCTCAGGGAAGAATATGACGTGCTTACCTG	1380
Db	1316	AGAGTCGTGGCCACAGGSGTACCAGCTCTCAGGGAAGAAGATATGATGTGCTTACCTG	1375
Qy	1381	GGGACAGAGGATGACACCTCCACCGGGCTGTGCGCATTTGAGCTCAGTCTGCTTGT	1440
Db	1376	GGGACAGAGGATGGACACCTCCACCGAGCAGTGGGATCGAGCTCAGCTCAGCTTCTT	1435
Qy	1441	GAGGATCTGGCTTGTTCAGAACACACAGCCGGTTGAGACATGAATTTGTACACAGAT	1500
Db	1436	GAAGATCTGGCTTATTTCCAGAGCCACAGCCAGTTTGAGAAATGTAATTTGTACACAGC	1495
Qy	1501	TGGCTCTGTGGCTCCCATCTGAGGTACACAAAGTGAACACCAAGCTGTGGCCGT	1560
Db	1496	TGGCTCTGTGTGGCTCCCATCTGAGGTGACAAAGTGAATTAACAACAACTGTGGCCGT	1555
Qy	1561	CTCCAGAGCTGCTCGGAGTGTATCTTGGCCAGGACCCCGTGTGGCGCTGGAGCTTCGG	1620
Db	1556	CTCCAGAGCTGCTCAGAGTGCATCTTGGCCAGGACCCAGCTCTGTGCTGGAGCTTCCGG	1615
Qy	1621	CTTTGATCTTGTGTGGCCACCGCGGAGCACCGGGATGGTTCAAGATATAGAGTCA	1680
Db	1616	CTGGATGAGTGTGTGGCCATGCGGGGAGCACCGAGGTTGGTCCAAGACATAGAGTCA	1675
Qy	1681	CGGATGTCCTCTTTGTGTCCAAGAAGACCTGGAGAACATCCCGTAGTGTGTTGAAGTT	1740
Db	1676	GCAGATGTCCTCTTTGTGTCTTAAGAGCCCTGGAGAACGTCAGCTAGTGTGTTGAAGTT	1735
Qy	1741	CCGGTGGCTACTGTGGCCACGTTGCTCTCCCATGTTCCCCAGTGTGCTTGGGCATCC	1800
Db	1736	CCCGTGGCTACAGCTGGCATGTGGTCTTGCCCATGTTCTCCAAGCTCAGCATGGGCATCC	1795
Qy	1801	TGTGTGTGGCACCAGCCAGTGGAGTGTGACTGTGCTCTCACTCCCCGGAGGATGACATAGAG	1860

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Db 1796 TGTGTGGACACAGCCAGTGGAGTGAATCACTCACTCACCCCGCGGGATGGAGTGGAG 1855
Qy 1861 GTGTGTGTGACCCAGGCGCATGGGCTTATGCTTGCAGTGTCAAGAGGTGGAGCC 1920
Db 1856 GTGTGTGTGACCCAGGCGCATGGGCTTATGCTTGTGAATGTCAAGAGGTGGGCA 1915
Qy 1921 GCCGCGGTGGTGTCTTATAGCTTGTGTGGGCGAGCCAGCGGGAGCCCTCAACCGG 1980
Db 1916 GCCCATGTGTGAGCAGCTTACAGCTTGTATGGGCGAGCCAGAGATGCTCCGAGCGG 1975
Qy 1981 GCCACACCGTGTGGGGCTGGATTTGGTGGCTTTCTCTGGGTGTCTTGCAGCATCC 2040
Db 1976 GCCCACAC- --AGTGGGGCGGGACTGGCTGGCTTCTTGGGGATTTCTCGCAGCATCC 2032
Qy 2041 CTCACTCTCCCTGATTGGTGCCTCAGCAGCGTGGCGACAGAGGGAGCTTCTAGCT 2100
Db 2033 CTGACTCTCATCTTGATGTGGCGGTCAAGCAGCGCGGACAGAGGAACTTCTGGCT 2092
Qy 2101 AGAGACAAGTGGCTTAGATCTGGGGCTCCACCTTCTGGGACCAAGCTATAGTCAG 2160
Db 2093 AGAGACAAGTGGCGCTGGACCTGGGGCTCCACCTTCTGGGACCAAGCTACAGCAA 2152
Qy 2161 GACCTCTCCTCTCTTGCCTGAAGATGAAGCGCTGCCCTGGCCCTGGGTAAAGCGGGC 2220
Db 2153 GACCTCTCCTCTCCTCTGAAGATGAGCGGTGGCGCTGGCGCTGGCCCAAGAGGGCG 2212
Qy 2221 AGTGGTTTGTGTGCTTCCCTCCACCTTCTCTGCTGGATTTCTGCCAAGCCAGCCAC 2280
Db 2213 AGTGGCTTGTGTGATTTCAACACCTTCTCTGCTGATCTTCCCAAGCCAGCCAC 2272
Qy 2281 ATCCGGCTCACTGGGGCGCTCTAGCCACGCTGTGATGAGACCTCCATCTA 2330
Db 2273 ATTCGGCTAATGGGGCTCTCTAGCCACATGTGATGAACATCCATCTA 2322
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RESULT 11

US-09-160-762-1

; Sequence 1, Application US/09160762A

; GENERAL INFORMATION:

; APPLICANT: David Michalovich

; APPLICANT: Trudy Rachel Doe

; APPLICANT: Philip David Hayes

; TITLE OF INVENTION: NOVEL COMPOUNDS

; FILE REFERENCE: GP-30036

; CURRENT APPLICATION NUMBER: US/09/160,762A

; CURRENT FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 2893

; TYPE: DNA

; ORGANISM: HOMO SAPIENS

US-09-160-762-1

Query Match 69.8%; Score 1626; DB 16; Length 2893;

Best Local Similarity 83.2%; Pred. No. 0;

Matches 1938; Conservative 0; Mismatches 275; Indels 117; Gaps 3;

```
Qy 1 ATGCTTGCAGGGCCGAGCGCCCGCGCGCGCGCGCGCGCGCTCGCGGTCTTTCCCTTC 60
Db 110 ATGCGGGCTCTGCTGGCGCGCGCGCGCGCGCGCGCGCGCTACAGCCTCGCGCTTC 169
Qy 61 CCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 170 CC-----GCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 214
Qy 121 GTCCCGCGCTCAGTGCCAGAACCTCGCTGCCCATCTCCAGAGGTGACTCTATCTACCC 180
Db 215 GTCCCGCGCTCGGTGCCAGAACCTCGCTTCCATCTCTGAGGCTGACTCTGCTCTACC 274
Qy 181 CGGTTTGAGCGGTCTCATACATAAAATFACCTCTGCTCTCTCTGCTGCTGCTGCTGCT 240
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Db 275 CGGTTCCAGTCCCTCACACATACAAATTAATCTCTGTCTCTCTGTGTGATCTCCTCCAC 334
Qy 241 ACACCTTACGTGCGTGACGGATAGCATCTTCGCTTTAAACCCCTCCCTCTCTCTGGGAA 300
Db 335 ACACCTTATGTGTGGCCCGGACACCATCTTCGCTTTATCCCTGCCCTTCTCAGGGAG 394
Qy 301 AGACCCCGAAGATCGACTGGATGGTACCTCAGACTCACAGACAGAACTCAGGAGAGAA 360
Db 395 AGACCCCGAGGATGACTGGATGGTCTCAGGCTCACAGACAGAACTGTAGGAAGAA 454
Qy 361 GGCAGAAGAGGAGGAATGTCAAAATTTTATCAGATTTCTCGCCATTTGTCAATGCCCTCT 420
Db 455 GGCAGAAGAG- ----- 466
Qy 421 CACCTCTCAGCTGCGGCACCTTCGCTTTTGTATCCGAAGTGGGGGTTATTTGATGTGTCC 480
Db 467 -----GATGTGTCC 475
Qy 481 AGTTTCCAGAGTTGAAAGACTTGAGAGCGCGCGGGGAAATGTCTTTTGTAGCAGCT 540
Db 476 AGGTTCCAGCAGGTTGAAAGACTTGAGAGTGGCGGGGAAATGTCTTTTGTAGCAGCT 535
Qy 541 CAACGGTCAGCAGCTGTAATGGCTGGGGCGCTCTCTACACGCGCAGCTGTGAAGACATTC 600
Db 536 CAGCGGTACAGCAGCTGTAATGGCTGGGGGGTCTCTATGTGCTCAGCTGTGAAAACATAC 595
Qy 601 CTGGGGACTGAGCCATCATCTCCGAGCTGTGGTGCAGCTGAGGACTGGATTCGAACA 660
Db 596 CTGGGGAGGAGCAATTTATCAGAGCAGTGGTGTGCGGAGAGCTGGATTCGAGACA 655
Qy 661 GAGACCTTGTCTCTGCTTAAATGCTCCAGCCTTTGTGCGAGCTATGGTCTCTGAGCCCA 720
Db 656 GATACCTTGCCTTCTGCTGACGCCGCCAGCTTTGTGCGAGCGCTGGCTTGTAGGCCA 715
Qy 721 GCTGAGTGGGGGATGAAGATGGAGCATGAATCTTTTCTTCTTCTTCTTCTTCTTCTTCT 780
Db 716 CCCAATGGGGGATGAAGATGGAGCAGCAAAATCTACTTCTTCTTCTTCTTCTTCTTCTT 775
Qy 781 CGAGTGTGTGACTCTCTATGAGCGCATCAAGTCCCAAGAGTGGCCGAGTGTGTCGGGG 840
Db 776 CGAGCATTTGACTCATAGAGCGCATTTAAAGTCCCAAGGTTGGCCGCTGTGTGTCGGGG 835
Qy 841 GACCTTGGGGCAGGAGAACCTTTACAGAGATGGAGCAGCTTTTCTTGAAGGCTGACCTG 900
Db 836 GACCTCGGGGCGGAGAACCTCTCAGCAGAGATGGAGCAGCTTTTGTGAAAGCTGACCTG 895
Qy 901 CTGTGCCAGGGCCGAGCATGGCGGCTTCCGGGTTCTGCGAGCTATGGCAGAGCTT 960
Db 896 CTGTGCCAGGGCCTGAGCATGGCGGCTTCCAGTGTCTGCGAGGATTTGCTGTGCTT 955
Qy 961 CGGCTCAGCTGAGGCGGGAAACCCCATCTTTTATGGATCTTTTCTCCAGTGGGAA 1020
Db 956 CGACTGAGCTTGGGCGAGGAGCTCCCATCTTTTATGGCATCTTTTCTCCAGTGGGAG 1015
Qy 1021 GGAGCTGCCATCTCTGCTGTGTGCTTCCGACCCCAAGACATCCGGGCGAGTGTCTGAAT 1080
Db 1016 GGGCTACTATCTCTGCTGTCTGCTTCCGACCAAGACATTTCCGACAGTGTCTGAAT 1075
Qy 1081 GGTCCCTTTAGAGACTTAAACATGACTGCAACAGGGAGCTGCCTGTCTATGGACAAACAG 1140
Db 1076 GGTCCCTTCAGAGAACTAAAACATGACTGCAACAGAGAGCTGCCTGTCTGAGCAATGAT 1135
Qy 1141 GTGCCCCAGCCAGACCTGGAGAGTGCATGCCAACAACATGAAGCTCCAGCAGTTTGA 1200
Db 1136 GTGCCCCAGCCAGACCTGGAGAGTGCATCAACAACAATGAAGCTCCGAGCTTGGC 1195
Qy 1201 TCCTCACTCTCCCTGCCAGACCGGTGCTCACTCTTATCAGAGACCACTCTCTCATGGAC 1260
Db 1196 TCATCTCTCTCCCTGCGCTGACCGGTACTCACTCTTATCCGGGACCACTCATGGAC 1255
Qy 1261 AGGCGCGTGTCCCGGCTGAGCGGCGCCCTGCTGTCTACTACAGATACAGCCTATCTC 1320
Db 1256 AGGCGAGTGTTCAGAGCTGATGGCGACCCCTGCTGTGCTACTACAGATACAGCCTATCTC 1315
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QY 1321 AGAGTCGTGGCCACACAGGTGACCGCTCTCAGGGAAGAAATATGACGTGCTTACCTG 1380
Db |||||
QY 1316 AGAGTCGTGGCCACACAGGTGACCGCTCTCAGGGAAGAGATGATGCTGCTTACCTG 1375
Db |||||
QY 1381 GGCACAGAGATGGACACCTCCACCGGCTGTGCCATTTGGAGCTCAGTCTAGTCTTG 1440
Db |||||
QY 1376 GGGACAGAGATGGACACCTCCACCGAGCAGTGCAGATCGAGCTCAGCTCAGCTCTT 1435
Db |||||
QY 1441 GAGGATCTGGCTTGTTCACAGACACAGCCGGTTGAGAGCATGAAATTTACACAGAT 1500
Db |||||
QY 1436 GAAGATCTGGCTTATTCAGAGCCACAGCAGTTGAGAACATGNAATTTACACAGC 1495
Db |||||
QY 1501 TGGCTCCTGGTGGGTCCCATCTAGTGTGACACAACTGAAACACAGCAACTGTGGCGT 1560
Db |||||
QY 1496 TGGCTCCTGGTGGGTCCCATCTAGTGTGACACAACTGAAACACAGCAACTGTGGCGT 1555
Db |||||
QY 1561 CTCCAGAGCTGCTCGAGGTATCTTGGCCACAGACCCCGTGTGGCCCTGGAGCTTCGG 1620
Db |||||
QY 1556 CTCCAGAGCTGCTCAGAGTGATCTTGGCCACAGACCCCGTGTGGCCCTGGAGCTTCGG 1615
Db |||||
QY 1621 CTGTATGCTGTGTGCCCCACAGCCCGGAGACCCGGGATGTTCAAGATATAGATCA 1680
Db |||||
QY 1616 CTGGATGAGTGTGGCCCATCGCGGGAGACCGAGGTTGGTCCAGACATAGATCA 1675
Db |||||
QY 1681 GCGGATGCTCTTTTGTGTCCAAAGAACCTGAGAACATCCCGTAGTGTGAAAGTT 1740
Db |||||
QY 1676 GCAGATGCTCTCTTTGTGTCTAAAGAGCCTGGAGAACGTCACAGTAGTGTGAAAGTT 1735
Db |||||
QY 1741 CCGGTGGCTACTGTGGCCACAGTGTCTGCTGCTATGTTCCCGAGTCTGCTTGGCATCC 1800
Db |||||
QY 1736 CCGGTGGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1795
Db |||||
QY 1801 TGTGTGTGACACAGCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
Db |||||
QY 1796 TGTGTGTGACACAGCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1855
Db |||||
QY 1861 GTGGTGGTGACCCAGGGGCCATGAGGGGTTATGCTTGGAGTGTGAGAGGGTGGAGCC 1920
Db |||||
QY 1856 GTGGTGGTGACCCAGGGGCCATGAGGGGTTATGCTTGGAGTGTGAGAGGGTGGAGCC 1915
Db |||||
QY 1921 GCCCGGTGGTGGCTTATGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1980
Db |||||
QY 1916 GCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1975
Db |||||
QY 1981 GCCACACAGTGTGGGGCTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
Db |||||
QY 1976 GCCACAC--AGTGGGGCGGACTGGCTGGCTTCTTCTTGGGATTTCTCGCAGCATCC 2032
Db |||||
QY 2041 CTCACCTCTCTCTGATTTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
Db |||||
QY 2033 CTGACTCTCATTTCTGATTTGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2092
Db |||||
QY 2101 AGAGCAAGTGGGCTTAGATGCTGGGGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160
Db |||||
QY 2093 AGAGCAAGTGGGCTTAGATGCTGGGGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2152
Db |||||
QY 2161 GACCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
Db |||||
QY 2153 GACCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2212
Db |||||
QY 2221 AGTGGTTTGGTGGCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
Db |||||
QY 2213 AGTGGTTTGGTGGATTTCTCAGCACCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2272
Db |||||
QY 2281 ATCCGGCTCAGTGGGGCTCTAGCCAGTGTGATGAGACCTTCCATCTA 2330
Db |||||
QY 2273 ATTGGCTTAACTGGGGCTCTCTAGCCACATGTGATGAACAATCCATCTA 2322
Db |||||
```

RESULT 12

US-09-808-665A-1

; Sequence 1, Application US/09808665A

; GENERAL INFORMATION:

```
; APPLICANT: David Michalovich
; APPLICANT: Trudy Rachel Doe
; APPLICANT: Philip David Hayes
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30036-Cl
; CURRENT APPLICATION NUMBER: US/09/808,665A
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/160,762
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 98300693.3
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 9816423.9
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 9816676.2
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2893
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; US-09-808-665A-1
```

Query Match 69.8%; Score 1626; DB 34; Length 2893;

Best Local Similarity 83.2%; Pred. No. 0;

Matches 1938; Conservative 0; Mismatches 275; Indels 117; Gaps 3;

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QY 1 ATGCTTGGCCAGGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
Db |||||
QY 110 ATGCGCGCCTCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 169
Db |||||
QY 61 CGCGCGCGCCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 214
Db |||||
QY 121 GTCCCGCGCTAGTGCCCAAGAACCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db |||||
QY 215 GTCCCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 274
Db |||||
QY 181 CGGTTTGGAGCTGCTCATACGTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db |||||
QY 275 CGGTTGCGAGTCCCTCAGACATACATATCTGTTCTCTCTGTTGATGCTGCTGCTGCTGCTGCT 334
Db |||||
QY 241 ACACCTTACGTCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Db |||||
QY 335 ACACCTTATGTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 394
Db |||||
QY 301 AGACCCCGAAGATCGACTGGATGGTACCTGAGACTCAGACAGACAGAACTGCGAGGAAGAA 360
Db |||||
QY 395 AGACCCCGCAGATTGACTGGATGGTTCCTGAGGCTCAGACAGAACTGTAGGAAGAA 454
Db |||||
QY 361 GCAAGAAAGAGGAGCAATGTCACAATTTTATCCAGATTCTGCCATTGTCAATGCTCT 420
Db |||||
QY 455 GCAAGAAAGAG----- 466
Db |||||
QY 421 CACCTCTCAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Db |||||
QY 467 -----GATGTGTC 475
Db |||||
QY 481 AGTTTCCAGCAGTTGAAAGACTTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
Db |||||
QY 476 AGTTTCCAGCAGTTGAAAGACTTGAGAGCTTGAGAGTGGCGCGCGCGCGCGCGCGCGCGCG 535
Db |||||
QY 541 CAACGCTCAGCAGCTGTAATGCTGGGCGCTCTCTACACCGCGCGCGCGCGCGCGCGCGCGCG 600
Db |||||
QY 536 CAGCGGTGAGCAGCTGTAATGCTGGGCGGCTCTCTATGCTGCCACTGTGAAAGAACTAC 595
Db |||||
QY 601 CTGGGAGCTGAGCCCATCATCTCCGAGCTGTGGGTGCGAGCTGAGAGCTGGATTCGAACA 660
Db |||||
QY 596 CTGGGAGCGGAGCCAAATATACAGAGCAGTGGGTGCGTGGCGAGAGCTGGATTCGAGCA 655
Db |||||
QY 661 GAGACCTTGTCTATCTGCGCTTAATGCTCCAGCCTTTGTGCGAGCTATGCTCTCGAGCCCA 720
Db |||||
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[illegible]

13256	AGCCAGTGTGTTCCAGCTGATGGCCACCCCTGCTGTCTACTACAGATACAGCCTATCTC	13131
Db		
1321	AGAGTCGTGGCCACAGGGTGACCAGGCTCTCAGGGAAAGAAATATGACGTGCTTACCTG	1380
Qy		
1316	AGATCTGTGGCCACAGGGTGACCAGGCTCTCAGGGAAAGAGTATGATGTGCTTACCTG	1375
Db		
1381	GGGACAGAGGATGGACACCTCCACCGGGCTGTGGCGCATTTGGAGCTCAGCTGCTGTTG	1440
Qy		
1376	GGGACAGAGGATGGACACCTCCACCAGGACAGTGGGATCGGAGCTCAGCTCAGCGTCTT	1435
Db		
1441	GAGGATCTGGCTTGTGTTCCAGAACCCACAGCCGGTTGAGAGCATGAANAATGTTACCAGGAT	1500
Qy		
1436	GAAGATCTGGCTTATTTCCAGAGCCACAGCCAGTTGAGAACATGAANAATGTTACCACAGC	1495
Db		
1501	TGGCTCTGTGGGCTCCCATCTAGAGTGAACAAGTGAACACCAAGCACTGTGGCCGT	1560
Qy		
1496	TGGCTCTGTGGCTCCCGTACTGAGGTGACACAGTGAATACAACCAACTGTGGCCGT	1555
Db		
1561	CTCAGAGCTGTCTGGAGTGTATCTCTGGCCACAGACCCCTGTGTGGCCTGGAGCTTCCCGG	1620
Qy		
1556	CTCAGAGCTGTCTCAGAGTGCATCTCTGGCCACGAGACCCAGTCTGTGCTGGAGCTTCCCGG	1615
Db		
1621	CTTGTATCTGTGTGGCCACGCGCGGGAGCACCCGGGATGGTTCAAGATATAGAGTCA	1680
Qy		
1616	CTGATGAGTGTGTGGCCCATGTCGGGGAGCACCGAGGGTGGTCCNAGACATAGAGTCA	1675
Db		
1681	GCAGATCTCTCTTTGTGTCCAAAAGAACCTGGAGAACATCCCGTAGTGTGTTGAAGTT	1740
Qy		
1676	GCAGATCTCTCTTTGTGTCTTAAAGAGCCCTGGAGAACCTCCAGTAGTGTGTTGAAGTT	1735
Db		
1741	CCGGTGGCTACTGTGGCCACAGTGGTCTTGCCATGTTCCCCAGTTCTGCCTGGGCATCC	1800
Qy		
1736	CCGTGGCTACAGCTGGCCATGTGGTCTTGCCATGTTCTCAAGCTCAGCATGGGCATCC	1795
Db		
1801	TGTTGTGGACACACCCAGCTGGAGTGACTGCGCTCACTCCCGGAGGGATGACCTAGAG	1860
Qy		
1796	TGTTGTGGCACACAGCCACGTGGAGTGACTGCACCTCACCCCCCGGGATGACCTGGAG	1855
Db		
1861	GTGTTGTGACCCAGGGGCCATGGGGCTTATGTCTTGCAGTGTCCAGGAGGTGAGGCC	1920
Qy		
1856	GTGTTGTGACCCAGGGGCCATGGGGCTTATGTCTTGTAATGTCCAGGAGGTGGGGCA	1915
Db		
1921	GCCCGCTGTGCTGCTTATAGCTTGTGTGGGCAGCCAGCGGGACCCCTCAAAACCGG	1980
Qy		
1916	GCCCATGTGTTAGCAGCTTACAGCTTGGTATGGGCAGCCAGCGAGATGCTCGAGCCGG	1975
Db		
1981	GCCACACACCTGTGGGGCTGGAATGTGTTGGCTTTCCTCTGGGTGTCTTGACAGATCC	2040
Qy		
1976	GCCACACACACCTGTGGGGCTGGAATGTGTTGGCTTTCCTCTGGGGATTCCTCGCAGCATCC	2032
Db		
2041	CTCACTCTCTCTGATTGTGCGCTCAGCAGCGTCCGGACAGAGGGAGCTTCTAGCT	2100
Qy		
2033	CTGACTCTCACTCTGATTGTGCGGTACAGCGAGCGGGTTCGCCCTGGCCCTTCTGGCT	2092
Db		
2101	AGACACAAGTGGGCTTAGATCTGGGGCTTCCACCTTCTGGGACCAACAAGCTATAGTCAG	2160
Qy		
2093	AGACACAAGTGGGCTTGGACCTGGGGCTTCCACCTTCTGGGACCAACAAGCTATAGTCAG	2152
Db		
2161	GACCTCTCTCTCTGCGCTGAAGATGAACGCTGCGCCCTGGCCCTGGGTAAAGCGGGC	2220
Qy		
2153	GACCTCTCTCTCTCTGCGCTGAAGATGAACGCTGCGCCCTGGCCCTGGGTAAAGCGGGC	2212
Db		
2221	AGTGGTGTGTTGGTGGCTTCCCTCCACCTTCTGCTGGATTCTTGTGCCAAAGAGGCC	2280
Qy		
2213	AGTGGCTTGGTGGATTCTCACCACTTCTGCTGATCTTGTGCCAAAGAGGCC	2272
Db		
2281	ATCCGGCTACTGGGGGCTCTAGCCACGTTGATGAGACCTTCCATCTA	2330
Qy		
2273	ATTTCGGCTACTGGGGCTCTCTAGCCACATGTGATGAACATCCATCTA	2322
Db		

Query Watch	69.8%;	Score 1626;	DB 16;	Length 2894;
Best Local Similarity	83.2%;	Pred. No. 0;		
Matches 1938;	Conservative	0;	Mismatches 275;	Indels 117; Gaps 3;
QY	1	ATGCTTGCCAGGCGCCGAGCGGCCCGCGGGGCCCCCGCGGCTCCGGTCTTCCTCCCTTC	60	
Db	110	ATGCGCGGCTCTGCTGCGGGGCCCCGCGGGGTCGCGGCGAGGCTACAGGCTTCGCCCTTC	165	
QY	61	CGCGCCGCGGTGCTGCTGCTGCTGGCGATACTAAGCGGCCCGGCTGTGGCGCGCG	120	
Db	170	CC-----GCTACTGCTGCTGGCGGTCTGAGCGGCCCGGTATCGGCGCGC	214	
QY	121	GTCCCCCGCTCAGTGCCCGAGAACCTCGCTGCCCATCTCCGAGGCTGACTCCTATCTCAAC	180	
Db	215	GTCCCCCGCTCGGTGCGCCAGAACCTCGCTTCCAATCTCTGAGGCTGACTCCTGTCTCACC	274	
QY	181	CGGTTTGCAGCGTCATAGTGACAATACTCTGCCTCTCCTTGTGGATCTGCCTCCAC	240	
Db	275	CGGTTGCGAGTCCCTCACACATACAATACTCTCTCTCTGTGGATCTGCCTCCAC	334	
QY	241	ACACTTTAGCTCGGTGCACGGGATAGCATCTTCGCTTTAAACCTTCCCTTCTCTGGGGAA	300	
Db	335	ACACTTTATGTTGGCGCCCGGGACACCATCTTCGCTTTATCCCTGCCCCCTCTCAGGGGAG	394	
QY	301	AGACCCCGAAGGATCGACTGGATGGTACCTGAGACTCACAGACAGAACTCGAGGAAGAAA	360	
Db	395	AGACCCCGAGGATTCAGCTGGATGGTTCCTGAGGCTCACAGACAGAACTGTGAGGAAGAAA	454	


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QY 961 CGGCTCAGCTGAGCGGGAAACCCCAATCTTTTATGGATCTTTTCTCCAGTGGAA 1020
Db 956 CGACTGAGCTTGGGCGAGGACTCCCATCTTTTATGGCATCTTTTCTCCAGTGGAG 1015
QY 1021 GGAGCTGCCATCTCTGCTGTGTGCTTCCGACCCCAAGACATCCGGGAGTGTGAAT 1080
Db 1016 GGGGCTACTCTCTGCTGTGTGCTTCCGACCAAGACATTCGGACAGTGTGAAT 1075
QY 1081 GGTCCCTTTAGAGAGCTAAACATGACTGCAACAGGGACTGCGCTGTCATGCACAACGAG 1140
Db 1076 GGTCCCTTCAGAGAACTAAACATGACTGCAACAGAGGACTGCGCTGTCGACACATGAT 1135
QY 1141 GTGCCCCAGCCAGACCTGGAGAGTGCATGCCAACAAACATGAAGCTCCAGAGTTTGA 1200
Db 1136 GTGCCCCAGCCAGACCTGGAGAGTGCATGCCAACAAACATGAAGCTCCGACACTTTGGC 1195
QY 1201 TCCCTCACTCTCCCTGCCAGACCGGCTGCTCACTTTATCAGAGACCACTCTCATGGAC 1260
Db 1196 TCATCTCTCTCCCTGCCAGCGGTACTCACTTTATCCCGGGACCCCACTCATGGAC 1255
QY 1261 AGGCCGCTGTTCGGGCTGAGCGCGGCCCTGCTGTGCTCACTACAGATACAGCTATCTC 1320
Db 1256 AGGCCAGTGTTCAGCTGATGGCCACCCCTGCTGTGCTCACTACAGATACAGCTATCTC 1315
QY 1321 AGAGTGTGGCCCAACAGGCTGACCAAGCTCTCAGGGAAAGATATAGCTGCTCTACCTG 1380
Db 1316 AGAGTGTGGCCCAACAGGCTGACCAAGCTCTCAGGGAAAGATATAGTGTCTCTACCTG 1375
QY 1381 GGGACAGAGGATGACACCTCCACGGGCTGTGGCATTTGAGCTCAGCTCAGTGTCTTG 1440
Db 1376 GGGACAGAGGATGACACCTCCACGGAGCTGCGGATCGGAGCTCAGCTCAGGCTTCTT 1435
QY 1441 GAGGATCTGGCTTTGTCACAGAACACAGCGGCTGAGAGCATGAATTTACACAGAT 1500
Db 1436 GAAGATCTGGCTTTATCCAGAGCCACAGCGGCTGAGACATGAATTTACACAGC 1495
QY 1501 TGGCTCCTGTGGCTCCCATCTAGGTGACAAAGTGAACACAGCAACTGTGGCGT 1560
Db 1496 TGGCTCCTGTGGCTCCCGTACTGAGGTGACAAAGTGAATACAACCACTGTGGCGT 1555
QY 1561 CTCAGAGCTGCTCGGAGTGTATCTGGCCACAGACCCCTGTGGCGCTGAGGCTTCGG 1620
Db 1556 CTCAGAGCTGCTCAGAGTGTATCTGGCCACAGACCCAGTCTGTGGCTGAGGCTTCGG 1615
QY 1621 CTTGATGCTGTGTGGCCAGCGCGGAGCACCGGATGCTTCAAGATATAGAGTCA 1680
Db 1616 CTGATGATGTGTGGCCATGCCGGGAGACCGAGGTTGTTCCAAAGACATAGAGTCA 1675
QY 1681 GCGGATGCTCTTTGTGTCCAAAGAAACCTGGAGAACATCCCGTAGTGTTTGAAGTT 1740
Db 1676 GCAGATGCTCTCTTTGTGTCTTAAAGAGCTGGAGAACGTCCTCCAGTAGTGTTTGAAGTT 1735
QY 1741 CCGGTGGCTACTGTGGCCAGCTGGTCTGCCATGTTCCCCCACTTCTGCTGGGCATCC 1800
Db 1736 CCCGTGGCTACAGCTGGCATGTGTGTGCTGTCATGTTTCCAAAGCTCAGCATGGGCATCC 1795
QY 1801 TGTGTGGCACACAGCCAGTGGAGTGACTCGCTCACTCCCGGAGGATGGACTAGAG 1860
Db 1796 TGTGTGGCACACAGCCAGTGGAGTGACTGCACTACCCCCGGGGATGGACTGGAG 1855
QY 1861 GTGTGTGTGACCCAGGGGCCATGGGGCTTATGCTTTCGAGTGTCTAGAGGGTGGAGCC 1920
Db 1856 GTGTGTGTGACCCAGGGGCCATGGGGCTTATGCTTGTGAATCTCAGGAGGGTGGGCA 1915
QY 1921 GCCCGCTGTGTGCTTATAGCTTGGTGGGGCAGCAGCGGGGACCTCAACCGG 1980
Db 1916 GCCCATGTGTGTAGAGCTTACAGCTTGGTATGGGGCAGCAGAGATGCTCCGAGCGG 1975
QY 1981 GCCCACACCGTGTGGGGCTGGATGGTGGCTTTCTCCTGGGTTCTTGTGCAGCATCC 2040
Db 1976 GCCCACAC ---AGTGGGGCGGGACTGGCTGGCTTCTTGTGGGGATTTCTCGCAGCATCC 2032
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QY 2041 CTCACCTCTCTCTGATTTGGTGGCGTCAGCAGCGTGGCGCACAGAGGGAGCTTCTAGCT 2100
Db 2033 CTGACTCTCTCATTTCTGATTTGGTGGCGTCAGCAGCGACGGCGCACAGAGGAACTTCTGGCT 2092
QY 2101 AGAGACAGGTTGGGCTTAGATCTGGGGCTCCACTTCTCTGGGACCAACAGCTATAGTCAG 2160
Db 2093 AGAGACAGGTTGGGCTTAGACTGGGGCTCCACTTCTCTGGGACCAACAGCTATAGTCAG 2152
QY 2161 GACCTCTCCTCTCTCTTCCCTTGAAGATGAACGGGTGGCGCTGGCTTGGTAAAGCGGGC 2220
Db 2153 GACCTCTCCTCTCTCTTCCCTTGAAGATGAACGGGTGGCGCTGGCTTGGTAAAGCGGGC 2212
QY 2221 AGTGGTTTGTGGCTTCCCTCCACCTTCTCTGCTGATTTTGGCCCAAGCCAGCCAC 2280
Db 2213 AGTGGCTTGTGGATTTCTACACCTTCTCTGCTTGTATCTTGGCCCAAGCCAGCCAC 2272
QY 2281 ATCCGGCTCACTGGGGCGGCTTAGCCACGCTGATGAGACTTCCATCTA 2330
Db 2273 ATTGGCTAATCTGGGGCTCTCTAGCCACATGTGATGAACATCATCTA 2322
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Search completed: September 26, 2003, 10:54:48
Job time : 6800.65 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1271.2	54.5	2082	1	PCT-US03-27411-47	Sequence 47, Appl
2	248.6	10.7	1914	1	PCT-US03-09929-1	Sequence 1, Appli
3	248.6	10.7	1914	1	PCT-US03-09929-7	Sequence 7, Appli
4	248.6	10.7	1914	1	PCT-US03-09929-9	Sequence 9, Appli
5	247.8	10.6	3112	1	PCT-US03-09929-5	Sequence 5, Appli
6	246	10.6	2739	1	PCT-US03-09929-11	Sequence 11, Appli
7	223.2	9.6	2049	1	PCT-US03-09929-3	Sequence 3, Appli
8	215.2	9.2	2589	1	PCT-US02-36071A-168	Sequence 168, App
9	215.2	9.2	4157	1	PCT-US02-36071A-167	Sequence 167, App
10	205.6	8.8	2586	1	PCT-US02-36071A-165	Sequence 165, App
11	205.6	8.8	2769	1	PCT-US02-36071A-164	Sequence 164, App
12	155.6	6.7	2705	1	PCT-US03-27411-44	Sequence 44, Appl
13	145	6.2	725	1	PCT-US03-27411-40	Sequence 40, Appl
14	62	2.7	1327	1	PCT-US03-09929-21	Sequence 21, Appl
15	62	2.7	1327	1	PCT-US03-17412-21	Sequence 21, Appl
16	62	2.7	1438	1	PCT-US03-09929-25	Sequence 25, Appl
17	62	2.7	1438	1	PCT-US03-17412-25	Sequence 25, Appl
18	62	2.7	1492	1	PCT-US03-09929-23	Sequence 23, Appl
19	62	2.7	1492	1	PCT-US03-17412-23	Sequence 23, Appl
20	62	2.7	1878	1	PCT-US03-09929-33	Sequence 33, Appl
21	62	2.7	1878	1	PCT-US03-17412-33	Sequence 33, Appl
22	62	2.7	1908	1	PCT-US03-09929-35	Sequence 35, Appl
23	62	2.7	1908	1	PCT-US03-17412-35	Sequence 35, Appl
24	62	2.7	1921	1	PCT-US03-09929-15	Sequence 15, Appl
25	62	2.7	1921	1	PCT-US03-17412-15	Sequence 15, Appl
26	62	2.7	1948	1	PCT-US03-09929-49	Sequence 49, Appl

; LOCATION: (1)..(1914)
PCT-US03-09929-9

[illegible]

Db	1151	ACGAGTGGGGCTCGGTGGAGCGCGCCCTGCTGCTGAAGAGGGGACCAACTTCACCC	12110
Qy	1322	GAGTCGTGGCCACAGGGTGACCAAGCCTCTCAGGGAAGAAATATGAGCTGCTCTACCTGG	13811
Db	1211	ACCTGGTGGCGACCGGGTTACAGGACTTGATGGAGCCACTATACAGTCTGTTTCATTG	12701
Qy	1382	GGACAGGATATGGACACTCCACGGGCTGTGGCATTGGAGCTCAGCTCAGTGTCTTTGG	14411
Db	1271	GCACAGGACGGCTGGCTGCTCAAGGCTGTGAGCCTGGGCGCTTACCTGATTTG	13301
Qy	1442	AGGATCTGGCCTTGTT---CCCAGAACACAGCGCGTTGAGAGCATGAATTTGTACACG	14981
Db	1331	AGGAGCTGCAGCTGTGTTTGACCAAGAGGCCCATGAGAAGCCTGGTGCTATCTCAGAGCAAGA	13901
Qy	1499	ATTGGCTCCTGGTGGGCTCCCATACTCAGGTGACACAAGTGAACACAGCAACCTGTGGCC	15581
Db	1391	AGCTGCTCTTTGGCGGCTCCGGCTCTCAGCTGGTGCAGCTGCCGTGGCCGACCTGCATGA	14501
Qy	1559	GTCTCCAGAGCTGTCGGAGTGTATCTTGGCGCCAGGACCCCGTGTGGCCCTGGAGCTTCC	16181
Db	1451	AGTATCGCTCTGTGACAGATGTGTCTCGCCGGGACCCCTATTGGCCCTGGAGCGTCA	15101
Qy	1619	GGCTTGANGCTTGTGTGGCCCAACGCCGGCGA	1649
Db	1511	ACACGACCGCTGTGTGGCGGTGGGTGGCCA	1541

RESULT 5

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PCT-US03-09929-5
: Sequence 5, Application PC/TUS0309929
: GENERAL INFORMATION:
: APPLICANT: Curagen Corporation, et al.
: TITLE OF INVENTION: THERAPEUTIC POLYPEPTID
: FILE REFERENCE: 21402-573B-061
: CURRENT APPLICATION NUMBER: PCT/US03/09929
: CURRENT FILING DATE: 2003-04-01
: PRIOR APPLICATION NUMBER: 60/368,996
: PRIOR FILING DATE: 2002-04-01
: PRIOR APPLICATION NUMBER: 60/369,980
: PRIOR FILING DATE: 2002-04-04
: PRIOR APPLICATION NUMBER: 60/370,381
: PRIOR FILING DATE: 2002-04-05
: PRIOR APPLICATION NUMBER: 60/370,969
: PRIOR FILING DATE: 2002-04-08
: PRIOR APPLICATION NUMBER: 60/371,002
: PRIOR FILING DATE: 2002-04-09
: PRIOR APPLICATION NUMBER: 60/372,002
: PRIOR FILING DATE: 2002-04-12
: PRIOR APPLICATION NUMBER: 60/384,297
: PRIOR FILING DATE: 2002-05-30
: PRIOR APPLICATION NUMBER: 60/386,816
: PRIOR FILING DATE: 2002-06-07
: PRIOR APPLICATION NUMBER: 60/389,123
: PRIOR FILING DATE: 2002-06-13
: PRIOR APPLICATION NUMBER: 60/402,207
: PRIOR FILING DATE: 2002-08-09
: Remaining Prior Application data removed -
: NUMBER OF SEQ ID NOS: 179
: SOFTWARE: Curaseq1ist version 0.1
: SEQ ID NO 5
: LENGTH: 3112
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (104)..(2602)
: PCT-US03-09929-5

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Query Match 10.6%; Score 247.8; DB 1; Length 3112;
Best Local Similarity 52.1%; Pred. No. 1.1e-57;
Matches 702; Conservative 0; Mismatches 627; Indels 18; Gaps 6;
Ov 312 GATCGACTGGTGTACTCTGAGACTCACACACAGAAAGGCAAG-----AA 368


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Db 500 AGGGCCATGCTGGGCTTCTTGGATGTGAGTGTACTCGGCCACACTCAACAACCTCC 559
Qy 602 TGGGACGTAGAGCCCATCTCCCGAGCTGTGGGTCGAGCTGAGGACTGGATTGCAACAG 661
Db 560 TGGGACGGACCCATATCTCGGTACATGGGGC---CCACACCTCCATGAAGACAG 616
Qy 662 AGACCTTGTCACTCTGGCTTAATGCTCCAGGCTTTGTGCGAGCTATGCTCTGAGCCCGAG 721
Db 617 AGTACCTGGCTTTTGGCTCAACGAACCTCACTTGTAGGCTCTGCCTATGTACTGTAGA 676
Qy 722 CTGAGTGGGGGATGAAGATGGAGCAGATGAATCTTTTCTTCAAGGAGACCTCC 781
Db 677 GTGTGGGAGCTTCAAGGGGACGACGACAAAGGCTACTTCTTCTCAAGGAGCGGGAG 736
Qy 782 GAGTGTGGAGCTCTATGAGCGCATCAAGGTCCCAAGAGTGGCCGAGTGTGTGGGGGG 841
Db 737 TGGAGTCCGACTGTATGCCGAGCAGGTGTGGTCTGTGTGGCCGCTGTGCAAGGGC 796
Qy 842 ACCTTGGGGGAGGAAGACCTTTCAGCAGAGATGGAGCAGCTTTCTTGAAGGCTGACCTGC 901
Db 797 ATATGGGGGGCGACGGACCTTCAGAGAGAAAGTGACACCTTCTCTGAAGCGCGGCTGG 856
Qy 902 TGTGCCAGGGCCGAGCATGGCCGGGCTCCGGGGTCTCGAGGCTATGCGAGCTTC 961
Db 857 CATGCTCTGCCCCGAACTGGCAGCTCTACTTCAACCAAGCTGCAGGCGATG---CACACCC 913
Qy 962 GGCCTCAGCCTGGAGCGGGAACCCCATCTTTTATGGGATCTTTTCCCTCCAGTGGGAAG 1021
Db 914 TGCAGGACACCTCTCGGCACACACCACTTCTTTGGGGTTTCAAGCAGAGTGGGTG 973
Qy 1022 GAGCTGCCATCTGTCTGTGTGCTGTCGACCCCAAGACATCCGGGCACTGCTGAATG 1081
Db 974 ACATGTACTGTGCGGCCATCTGTGAGTACCAGTTGGAAGAGATCCAGCGGTGTTGAGG 1033
Qy 1082 GTCCCTTTAGAGACTAAACATGACTGCAACAGGGGACTGCCTGTCTATGACACACGAGG 1141
Db 1034 GCCCTATAGAGAGTACCATGAGGAAGCCCAAGAGTGGGACCGCTACACTGACCCCT---G 1090
Qy 1142 TGCCCCAGCCAGAGCTGGAGAGTGCATCGCCCAACACATGAAGCTCCAGCAGTTTGGAT 1201
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Db 1271 ACCTGTGGCCAGCGGTACAGGACTTGATGGAGCACCTATACAGTGTGTCTATTG 1330
Qy 1382 GGACAGAGATGGACACCTCACCGGGCTGTGCGCATTTGGAGCTCAGCTCAGTGTCTGG 1441
Db 1331 GCACAGGAGGGGTGGCAGCTCAAGGCTGTGAGCCTGGGGCCTGGGCTTCACTGATTG 1390
Qy 1442 AGGATCTGGCTTGT 1457
Db 1391 AGGAGCTGCAGCTGTT 1406
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RESULT 8

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PCT-US02-36071A-168
; Sequence 168, Application PC/TUS0236071A
; GENERAL INFORMATION:
; APPLICANT: Sagres Discovery
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000142
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; CURRENT APPLICATION NUMBER: PCT/US02/36071A
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 168
; LENGTH: 2589
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-36071A-168
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Query Match          9.2%; Score 215.2; DB 1; Length 2589;
Best Local Similarity 48.9%; Pred. NO. 9.7e-49;
Matches 747; Conservative 0; Mismatches 748; Indels 33; Gaps 5;

Qy 136 CCCAGAACCTCGCTGCCCATCTCCGAGGCTGACTCTCTATCTCACCCGGTTCGACGCGTCT 195
Db 76 CCCATACCCCGATCACCTGGGAGCACAGAGAGTGCACCTGGTGCAGATTTTCATCAGGCCA 135
Qy 196 CATACGTACAATTAATCTCTGCTCTCTCTTGTGGATCTGCTCTCCCTCCACACACTTTTACGTCGT 255
Db 136 GACATCTACAATACTACTCAGCCTTGTCTGCTGAGCGAGGACAAGGACACCTTGTACATAGT 195
Qy 256 GCACGGGATAGCATCTTCGCTTTTAACTCCCTCCCTCTCTGCGGGAAGACCCCGAAGATC 315
Db 196 GCCCGGAGGGGGTCTTCGCTGTGAACGACTCAACATCTCCGAGAAGCAGCATGAGGTG 255
Qy 316 GACTGGATGTPACCTGAGACTCAGACAGAACTGCAAGAAAGGAAGCAAG---AAACAG 372
Db 256 TATTGGAAGGTCTCAGAAGACAAAAGCAAAATGTGCAGAAAGGGGAATCAAAACAG 315
Qy 373 GACAAATCTCAAAATTTTATCCAGATTCCTGCCAATTCCTCAATTCCTCTCAGCTCTCAGC 432
Db 316 ACAGAGTCCCTCAACTACATCCGGTGTGCGAGCACTCAGCGCCACTTCCCTTTACGTG 375
Qy 433 TCGCGCACTTCGCTTTTGATCCGAAGTGCAGGGTATTATGATGTGTCAGTTTCAGCAG 492
Db 376 TGTGGGACCAACGATTCAGCGCGCTGTGACCACTGAACTTAACTTCCTTTAAGTTT 435
Qy 493 GTTGAAGACTTTGAGAGCGCGGGGAAATGTCTCTTTGAGCCAGCTCAACGGTCACGA 552
Db 436 CTGGGAAATTAAGATGGCAAGGAAGATGTCTCTTTGACCCAGCAGCTACACA 495
Qy 553 GCTGTAATGGTGGGGCGCTCTCTACACCCCACTGTGAAGAACTTCTCTGGGGACTGAG 612
Db 496 TCCGTGATGTTGATGGAGAACTTATTCGGGGACGTCGTATATAATTTTGGGAAGTCAA 555
Qy 613 CCCATCATCTCCGAGCTGTGGTGCAGCTGAGGACTGGATTCGAACAGACCTTGTCA 672
Db 556 CCCATCATCTCCGAAATTTCTCCACAGTCTCTGAGGACAGAATATGCAATCC----610
Qy 673 TCCTGGCTTAATGTCTCCAGCCTTGTGCGAGTATGCTCTGAGCCAGCTGAGTGGGG 732
Db 611 -CTTGGCTGAACAGCCCTAGTTTGTGTTGCTGACGTGATCCGAAAAGCCAGCAGCAGC 669
Qy 733 GATGAAGATGGAGCAGTGAATCTTTTCTTTCACGAGACCTCCCGAGTGTGGAC 792
Db 670 CCCGAGCGGAGGATGACAGGCTCTACTTCTTCTTTCAGGAGGTCTCTGTGAGTATGAG 729
Qy 793 TCCTATGAGCGCATCAAGTCCCAAGAGTGGCCCGAGTGTGTGGGGGAGCTTGGGGGC 852
Db 730 TTTGTGTTTCAAGGCTGTATCCCGGATAGCAAGAGTGTGCAAGGGGAGCAGGCGGC 789
Qy 853 AGGAAGACCTTCAGCAGAGATGGAGCAGTTCCTGAAGGCTGACCTCTGTGCCCCAGG 912
Db 790 CTGAGGACCTTGCAGAGAAATGGACCTCTCTCTGAAGCCCGACTCATCTGCTCCCGG 849
Qy 913 CCCGAGCATGGCCGGCTCCGGGCTTCTGAGGCTATGCGAGCTTTCGGCCTCAGCCT 972
Db 850 CCAGACAGCGCTTGGTCTTCAATGTGCTGCGGGATGTCCTGCTGCTCAGGTG---CCCG 906
Qy 973 GGAGGGGAACCCCATCTTTTATGGGATCTTTTCTCTCCCACTGGGGAAGAGAGCTGCCATC 1032
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Qy 1084 CCCTTTAGAGAGCTAAACATGACTGCAACAGGGGACTGCCTGTGTCATGGACAAGAGGTG 1143
Db 1027 ATGCAGAGACCACAGTGGAGCAGTCCACACCAAGTGGGTGCGGTATAATATGGCCGGTA 1086
Qy 1144 CCCAGCCCAAGCTGGAGAGTGCATGCCCAACACATGAAGCTCCAGCAGTTTGGATCC 1203
Db 1087 CCAAGCCGCGCTGGAGCGTGCATCGACAGCGGCGCGCCGCAACTACACCAGC 1146
Qy 1204 TCACCTCTCCCTGCCAGACCGGTGCTCACCTTTATCAGAGCACCCCTCTCATGACACAGG 1263
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Db 1327 ACAGACGGGAGCTCTCAAGAAGCAATAGCCTCGAGCAGCTGTTCACATCATCGAG 1386
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Db 1567 AGCCCGCCACAGCAGCTGCGTGGCTC 1594
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; Sequence 167, Application PC/TUS0236071A
; GENERAL INFORMATION:
; APPLICANT: Sagres Discovery
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000142
; CURRENT APPLICATION NUMBER: PCT/US02/36071A
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 167
; LENGTH: 4157
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-36071A-167
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Best Local Similarity 48.9%; Pred. No. 1.2e-48;
Matches 747; Conservative 0; Mismatches 748; Indels 33; Gaps 5;
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Db 163 CCCATACCCCGGATCACCTGGGAGCACAGAGAGGTGCACCTGGTGCACTTTTCATGAGCCA 222
Qy 196 CATAGCTACAATTAATCTGCTCTCTCTCTGCTGATCCTGCTCCACACACTTTAGCTCCGT 255
Db 223 GACATCTACAATTAATCTGCTGCTGAGCGAGGACAAGGACACCTTTGTACATAGGT 282
Qy 256 GCAGCGGATGATGATCTTCGCTTTAACCTTCCCTTCTCTGGGGAAGACCCCGGAAGATC 315
Db 283 GCCCGGAGGCGGTCTCGCTGTGAACCACTCAACATCTCCGAGAAGCAGCATGAGGTG 342
Qy 316 GACTGGATGATGCTGAGACTACAGACAGAACTGACAGAAAGGCAAG---AAGAG 372
Db 343 TATTGAAAGGTCTCAGAAAGCAAAAATGTGCAGAAAGGGGAAATCAAAACAG 402
Qy 373 GACGAATGTCACATTTTATCCAGATTTCTGCCATTTGTAATGCTCTCACCTCTCTCAGC 432
Db 403 ACAGAGTCCCTCAACTACATCCGGGTGCTGAGCCCACTCAGCCCACTTCCCTTTACGTG 462
Qy 433 TCGCGCACTTCGCTTTTATCCGAAGTCCGGGTATTGATGTGTCCAGTTTCCAGCAG 492
Db 463 TGTGGACCAACGCATTCACCGGCTGTGACCACTTGAACATCTCTTTAAGTTT 522
Qy 493 GTTGAAGACTTTGAGAGCGCGGGGAAATGTCTTTTGTAGCCAGCTCAACAGGTGACGA 552
Db 523 CTGGGAAAAATGAAGATGGCAAGAGAGATGTCTCTTTGACCCACACAGCTACACA 582
Qy 553 GCTGTAATGGCTGGGGGCTCTCTACACCCCACTGTGAAGAACTTCTCTGGGACTGAG 612
Db 583 TCCGTGATGGTGTGAGGAACTTTATTCGGGGAGCTGCTATTAATTTTGGGAAGTGA 642
Qy 613 CCCATCATCTCCCGAGCTGTGGTGCAGCTGAGGACTGGATTTCGAACAGAGACCTTGTCA 672
Db 643 CCCATCATCTCCCGAATTTCTCCACAGTCTCTGAGGACAGATATGCAATCC---- 697
Qy 673 TCTGGCTTAATGTCTCCAGCCTTTGTGCGAGCTATGTCCTGAGCCCACTGAGTGGGG 732
Db 698 -CTTGGCTGAACGAGCCTTAGTTCTGTTGACGTGATCCGAAAAAGCCACAGCAGC 756
Qy 733 GATGAAGATGAGAGCATGAATCTTTTCTTCAGGAGACCTCCCGAGCTTGGAC 792
Db 757 CCGACGCGGAGGATGACAGGCTCTACTTCTTTCACGGAGGTCTCTGTGGAGTATGAG 816
Qy 793 TCTATGAGCGCATCAAGGTCCCAAGAGTGGCCCGAGTGTGTGCGGGGAGACTTGGGGC 852
Db 817 TTTGTGTTCCGGGTCTGATCCCAGGATAGCAAGAGTGTCAAGGGGAGCAGGCGGC 876
Qy 853 AGGAAGACCTTTACGACAGATGAGAGCTTTTCTGAAGGTGACCTGCTGTGCCCCAGGG 912
Db 877 CTGAGGACCTTGCAGAAGAAATGGACCTCTCTCTGAAAGCCGAGCTCATCTGCTCCGG 936
Qy 913 CCCGAGATGCCCGGCTCCGGGTTCTGAGGCTATGCGAGCTTGGCAGACTTCCGCTCAGCT 972
Db 937 CCAGACATGGGCTTGGTCTTCAATGTGCTGGGAGTGTCTGCTGCTCAGGTC---CCG 993
Qy 973 GGAGCGGAACCCCATCTTTTATGGGATCTTTTCTCCAGTGGGAAGAGCTGCCATC 1032
Db 994 GGCCTGAAGTGCCTGTGTTCTATGCACTTTCACCCCACTGTAACACAGTGGGGCTG 1053
Qy 1033 TCTGCTGTGTGTC-----TTCCGACCCCAAGACATCCGGGAGTGTGTAATGTT 1083
Db 1054 TCGGCACTGTGCGCTTACAACCTGTCCACAGCCGAGAGGTCTTCTCCACCGGAAGTAC 1113
Qy 1084 CCTTTAGAGCTAAACATGACTGCAACAGGGGACTGCTCTGTCATGGACAACAGGTG 1143
Db 1114 ATGCAGACCAACAGTGGAGCAGTCCCAACCAAGTGGGTGCGGTATAATGCGCCGTA 1173
Qy 1144 CCCAGCCAGACCTGGAGGTGCATCGCAACAACATGAAGCTCCAGCAGTTTGGATCC 1203
Db 1174 CCCAGCCGCGCTTGGAGGTGCATCGACAGGAGCAGCGGCGCCCACTACACCAGC 1233
Qy 1204 TCACTCTCCCTGCCAGACCGGTGCTCACCTTTATCAGAGACCAACCCCTCTCTATG 1263
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Db 1234 TCCTTGAATTGCGACACAGAGCGTGCAGTTCGTTTAAAGACACACCTTTGATGATGAC 1293
QY 1264 CCGGTGTTCCGGCTGACGGCCGCCCTGCTGCTCAGTACATACAGCTATCTCAGA 1323
Db 1294 TCGGTAACCCCAATACACACAGCCCGCGGTTAATCAAGAAAGATGTGAATACACCCAG 1353
QY 1324 GTGCTGGCCACAGAGGTGACAGCTCTCAGGGAAGAAATATAGCTGTACCTGGGG 1383
Db 1354 ATCGTGGTGGACGGGACCCAGGCCCTGGATGGAGCTGTCTATGATGATGTTGTCAGC 1413
QY 1384 ACAGAGGATGGACACCTCCACCGGCTGTGCGATTGGAGCTCAGTCTAGTCTTGGAG 1443
Db 1414 ACAGACGGGGAGCTGTGCACAAAGCCATCAGCCTCGAGCAGCTTTTACATCATCGAG 1473
QY 1444 GATCTGGCTTGTTCACAGAACACAGCCGGTGTAGAGCATGAATTTGTA----- 1493
Db 1474 GAGACCCAGCTCTTCAGAGACITTGAGCCAGTCCAGACCCCTGCTGCTTCAAGAAG 1533
QY 1494 --CCAGATGGCTCTGCTGGGCTCCCATATCTAGAGTGACACAAAGTGAACACCAAGCAAC 1551
Db 1534 GGCACAGGTTTGTCTATGCTGCTTAACCTGGGCGTGGTCCAGGCCCGCTGGGCTTC 1593
QY 1552 TGTGGCCGCTCCAGAGCTGCTCGGAGTGTATCTTGGCCAGGACCCCGTGGCGCTGG 1611
Db 1594 TGTGGGAAGCAGCGCACCTGCGAGGAGCTGTGCTGGCGGGAGCCCTACTGCGGCTGG 1653
QY 1612 AGCTTCGGCTTGTATGCTTGTGGGCC 1639
Db 1654 AGCCGCCACAGCAGCACTGCGTGGCTC 1681

RESULT 10

PCT-US02-36071A-165

; Sequence 165, Application PC/TUS0236071A

; GENERAL INFORMATION:

; APPLICANT: Sagres Discovery

; APPLICANT: Morris, David W.

; APPLICANT: Engelhardt, Eric K.

; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER

; FILE REFERENCE: 529452000142

; CURRENT APPLICATION NUMBER: PCT/US02/36071A

; CURRENT FILING DATE: 2002-11-08

; PRIOR APPLICATION NUMBER: US 10/052,482

; PRIOR FILING DATE: 2001-11-08

; NUMBER OF SEQ ID NOS: 241

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 165

; LENGTH: 2586

; TYPE: DNA

; ORGANISM: Mus musculus

PCT-US02-36071A-165

Query Match 8.8%; Score 205.6; DB 1; Length 2586;

Best Local Similarity 49.2%; Pred. No. 4,3e-46;

Matches 733; Conservative 0; Mismatches 724; Indels 33; Gaps 6;

QY 174 TCTACCCCGTTTGCAGCTCTCATACGTACAAATTAATCTGCTCTCCTTGTGGATCCTGC 233
Db 114 TCTGTGCACTTTCACAGCCAGGCATCTTTAACTACTCGGCTTGTCTGATGAGTGAGGA 173
QY 234 CTCACACACACTTTAGTGGGTGCACGGGATAGCAATCTTGGCTTTAAACCCCTCCCTTCTC 293
Db 174 CAAAGACACTCTGTATGTAGGCGCCGGGAAGCAGTCTTTGCAGTGAATGCGCTGAACAT 233
QY 294 TGGGAAGACCCCGAAGGATCGACTGGATGGTACTGAGCTCAGACACAGAACTGGAG 353
Db 234 CTCTGAGAGCAACATGAGGTATATTTGGAAGCTCTCTGAAGACAAAAATCCAAAGTGTGC 293
QY 354 GAAGAAGGCAAA--GAAGAAGGAGCAATGTACAAATTTTATCCAGATTTCTCGCCATGT 410
Db 294 AGAAGAAGGGAATCAAGCAGACGCAATGCCTAACTACATTCGAGTACTACACCCACT 353

QY 411 CAATGCTCTCACCTCCTCACGTGGCGCACCTTTCGCTTTTGATCCGAAGTGGCGGTTAT 470
Db 354 AAGCAGCACTTCCCTCTATGTGTGGGACCAATGCTTCCAGCCACACCTGTGACCACT 413
QY 471 TGNATGTCCAGTTTCCAGCAGGTTGAAAGACTTTAGAGCGGCGCGGGGAAATGTCTTT 530
Db 414 GAATTTGACATCTTCAAGTTTCTGGGAAAAGTGAAGATGGCAAGGAAGATGCCCCCTT 473
QY 531 TGAGCCAGCTCAACGCTCAGCAGCTGTAATGGCTGGGGCGTCTCTACACCCCACTGT 590
Db 474 CGACCCCGCCACAGCTACACATCAGTCATGGTTGGGGGAGCTCTACTCTGGGAGCTC 533
QY 591 GAAGAATTTCTTGGGAGCTAGCCCCATCATCTCCGAGCTGTGGGTGCGAGCTGAGGACTG 650
Db 534 CTATAATTTCTTGGGAGTGAACCCATCATCTCTCGAACTCTTCCACAGTCCCTTGAG 593
QY 651 GATTCGAACAGAGACCTTGTCTCCTGCGCTTAATGCTCCAGCTTTTTCGACGCTATGT 710
Db 594 G-----ACGGAGTATGCCATCCGTTGGCTGAACAGAGCTAGTCTCTTGTCTGACGT 647
QY 711 CCTGAGCCCGAGCTGAGTGGGGGATGAAGATGGAGACGATGAATCTTTTTCCTTCAC 770
Db 648 GATCCAGAAAAGCCACAGATGGTCCGAGGTTGAAGATGACAAGTCTACTTCTTTTAC 707
QY 771 GGAGACCTCCCGAGTGTGGACTCTTATGAGCGCATCAAGGTCCCAAGAGTGGCCCGAGT 830
Db 708 GGAGGTATCCGTGGAGTACGAATTCGTCTCAAGTTGATGATCCCGAGTTGCCAGGT 767
QY 831 GTGTGGGGGAGCTTGGGGGAGGAGACCTTTCAGCAGAGATGGACACGCTTCTCGAA 890
Db 768 GTGCAAGGGCGACAGGGCGGCTGCGGACTTTGCAAAAAAAGTGGACCTCTCTCTTAA 837
QY 891 GGCTGACCTGCTGTGCCAGGGCGGAGCATGGCGGGCTCCGGGTTCTTCGACGCTAT 950
Db 828 GGCAGGCTGATCTGCTCAAGCCACAGAGTGGCTGGTCTTCAACATACTTCAGGATGT 887
QY 951 GGCAGAGCTTCCGCTCAGCTTGGAGCGGAACCCCATCTTTATGGAGTCTTTTCCTC 1010
Db 888 GTTTGTGTGAGGGC---CCCGGGCTCAAGAGAGCTGTGTTCTATGCGGTCTTCAACC 944
QY 1011 CCAGTGGGAAGAGCTGCCATCTCTGCTGTGTGCTTCCGACCCCAAGACATCCGGC 1070
Db 945 ACAGCTGAACAATGTGGGTCTGTGAGCGGTGCGCTTACACACTGGCCACGCTGGAGGC 1004
QY 1071 AGT-----GCTGAATGCTCCTTTAGAGAGCTAAA--ACATGACTGCAACAGGGGACT 1121
Db 1005 ACTCTTCTCCCGTGGAAAGTACATCAGAGTGCCACAGTGGAGCAGTCTCACACCAAGT 1064
QY 1122 GCCTGTGACAGACAGAGGTGCCCGAGCCAGACCTGGAGAGTGGATCGCCCAACAACT 1181
Db 1065 GGTGGGCTACAATGGCCAGTCCCACTCCCGAGCTGGAGGCTGTATCGACAGTGGGC 1124
QY 1182 GAAGCTCCAGAGTTTGGATCTCTCCTGCCAGACCGGCTGCTCACCTTTATCAG 1241
Db 1125 CCGGGAGCCAACTACACCAGCTCCTTGAATCTCCAGACAAAACACTGCAGTTGTAAA 1184
QY 1242 AGACACCCCTCTCATGGAGCGGCTGTTCGGGTGCTGAGCGCGCCCTCTGTGCTAC 1301
Db 1185 AGACACCCCTTTGATGGATGACTCAGTGACCCCGATAGACACAGACCCCAAGCTGATCA 1244
QY 1302 TACAGATACAGCTTATCTCAGAGTGTGGCCCAAGGGTGGACGCTCTCAGGGAAGA 1361
Db 1245 AAAAGATGTAACTACACCCAGATAGTGGTAGACAGGCCACCGGCTGGATGGGACTTT 1304
QY 1362 ATATCAGTGTCTACCTGGGACAGAGATGGACACCTCCACCGGCTGTCGATTTGG 1421
Db 1305 CTACAGCTGATGTTTCATCAGCAGACAGCCGGGAGCTGTGCATAAGAGTCTATCTTAC 1364
QY 1422 AGCTCAGCTCAGTCTTGGAGGATCTGGCCCTTGTTCACAGAACACACAGCCGCTGAGAG 1481
Db 1365 AAAAGAGGTGCTATCGAGGAGACCACTCTTCCGGGACTTTTGAACCGGCTCTTAAC 1424
QY 1482 CATG-----AAATGTACACGATTGGCTCTCTGGTGGGCTCCCACTACTGAGGT 1529

Db 1425 TCTGCTGCTATCGTCAAGAAGGGGAGGAAGTTTGTCTATGAGGCTCCAACTCTGGAGT 1484
QY 1530 GACACAAAGTGAACACCAAGTGGCGGCTCCAGAGCTGCTCGGAGTGTATCCTGCG 1589
Db 1485 GGTCAAGCGCCCTGGGATCTCTCGAAGACACGGTAGCTGTGAAGACTGTGTGTAGC 1544
QY 1590 CCAGGACCCCGTGTGGCGCTGGAGCTTCCGGCTTGATGCTTGTGTGGGCC 1639
Db 1545 ACGGGACCCCTACTGTGCTGGAGCCAGCCATCAAGGCTGTGTATCCC 1594

RESULT 11

PCT-US02-36071A-164
; Sequence 164, Application PC/TUS0236071A
; GENERAL INFORMATION:
; APPLICANT: Sagres Discovery
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000142
; CURRENT APPLICATION NUMBER: PCT/US02/36071A
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 164
; LENGTH: 2769
; TYPE: DNA
; ORGANISM: Mus musculus
PCT-US02-36071A-164

Query Match 8.8%; Score 205.6; DB 1; Length 2769;
Best Local Similarity 49.2%; Pred. No. 4.4e-46;
Matches 733; Conservative 0; Mismatches 724; Indels 33; Gaps 6;

QY 174 TCTACCCCGGTTTGACGGGTCTCATACGTACAAATTAATCTGCTCTCTCTGTTGGATCCCTGC 233
Db 174 TCTGGTGCAGTTTCAAGCCAGGCGATCTTTAACTACTCGGCCCTTGTGATGAGTGAGGA 233
QY 234 CTCCACACACTTTACGTCGGGTGACGGGATGATCATCTTCGCTTTAAACCTCCCTCTCTC 293
Db 234 CAAGACACACTCTGTATGTAGGCGCCGGGAGCAGCTCTTGCAGTGAATGCGCTGAACAT 293
QY 294 TGGGAAAGACCCCGAAGGATCGACTGTGATGATGATGATGATGATGATGATGATGATG 353
Db 294 CTCTGAGAGCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 353
QY 354 GAAGAAAGGCAA--GAAAGAGGAGCAATGTACAAATTTTATCCAGATTTCTGCCATTTGT 410
Db 354 AGAGAAGGGGAAATCAAGACAGACGGAATGCTTAACTACATTTCCAGTACTACACCCACT 413
QY 411 CAATGCCCTCCTACCTCTCAGTGGGACCTTTCGCTTTGATCGAAGTGGGGGTTAT 470
Db 414 AAGACGACACTTCCCTCTATGTGTGGGACCAATCGTTTCCAGCCACCTGTGACCACT 473
QY 471 TGATGTGTCAGTTTTCAGCAGGTTGAAAGACTTCAGAGCGCGCGGGGAAATGTCCTT 530
Db 474 GNACTGTACATCTTCAAGTTTCTGGGAAAGTGAAGATGAAGATGCAAGGAAGATGCCCTT 533
QY 531 TGAGCCAGCTCAACGGTCAAGCTGTATATGGCTGGGGCGCTCTCTACACCGCCACTGT 590
Db 534 CGACCCGCCACACACTACACATCAGTCATGTTGGGGCGAGCTCTACTCTGGGACGTC 593
QY 591 GAAGAACTTCTGGGAGTGAAGCCCATCATCTCCGAGCTGTGGGTGAGCTGAGACTG 650
Db 594 CTATAATTTCTGGGAGTGAAGCCCATCATCTCTGAAACTTCTCCACAGTCCCTTGAG 653
QY 651 GATTCGACAGAGACCTTGTCTATCTCTGCTTAATCTCTCAGCCTTTGTGCGAGTATGGT 710
Db 654 G-----ACGGAGTAGCCATCCCGTGGCTGACAGAGGCTAGCTTCGCTTTGCTGAGCT 707

QY 711 CCTGAGCCAGCTGAGTGGGGGATGAAGATGAGAGCATGAGAGCATGAGAGTCTTTTTTTCTTAC 770
Db 708 GATCCAGAAAAGCCCGAGATGGTCCGAGGGTGAAGATGACAAGGTCTACTTCTTTTTTAC 767
QY 771 GGAGACCTCCCGAGTGTGGAGTCTCTATGAGCGCATCAAGGTCCCAAGAGTGGCCGAGT 830
Db 768 GSAGGTATCCGTTGGATACGAATTCGTCTTCAAGTTGATGATCCCGCGAGTGGCCAGGT 827
QY 831 GTGTGCGGGGACCTTGGGGGAGGAAGACCTTCCAGCAGAGATGAGAGCATGAGAGTCTTCTGAA 890
Db 828 GTGGAAGGGCGACAGGGGCGCTCGGACTTTGCAAAAAGTGGACCTCTCTCTCTCTCTCTCT 887
QY 891 GGCTGACCTGTGTGCCAGGCGCGAGCATGGCGGGCTCCGGGGTTCTCAGAGCTAT 950
Db 888 GSCCAGGCTGATCTGCTCAAGCCAGACAGTGGCTGTCTTCAACATATCTTCTCAGAGTGT 947
QY 951 GGCAGAGCTTCCGGCTCAGCTGGAGCGGGAACCCCATCTTTTATGGATCTTTTCTCTC 1010
Db 948 GTTGTGTGTAGGGC---CCCGGGCTCAAGGAGCTGTGTCTATGCGGTCTTCAACCC 1004
QY 1011 CCAGTGGGAAGGAGTGGCATCTCTGCTGTGTGTGCTTCCGACCCCAAGACATCGGGC 1070
Db 1005 ACAGCTGAACATGTGGTCTGTACGGGTGTGCGCTTACACACTGGCCACCGTGGAGC 1064
QY 1071 AGT-----GCTGAATGTCTCTTTAGAGAGCTAAA--ACATGACTGCAACAGGGAGCT 1121
Db 1065 AGTCTTCTCCCGTGGAAAGTACATGCAGAGTCCACAGTGGAGAGTCTCTCACACCAAGTG 1124
QY 1122 GCCTGTATGGACAACAGAGTGGCCCGCCAGCTGGAGAGTGGAGAGTGCATGCCCAACACAT 1181
Db 1125 GGTGCGCTACAAATGGCCAGTGGCCACTCCCGGAGCTGGAGGCTGTATGCAGAGTGAAGC 1184
QY 1182 GAACTCTCAGCAGTGTGGATCCTCACTCTCCTGCGCAGACCCGCTGCTCACTCTCTATCAG 1241
Db 1185 CGGGCAGCAACTACACAGCTCTTGAATCTCCAGACAAAACACTGACGCTTTGTATAA 1244
QY 1242 AGACACACCTCTCATGGAGCGCGGTGTCCCGGCTGACGGCGCGCCCTCTGCTGTCAC 1301
Db 1245 AGACACACCTTTGATGGATGACTCAGTGAACCCGATAGACAACAGACCCCAAGCTGATCAA 1304
QY 1302 TACATATACAGCTTATCTCAGAGTGTGGCCCAAGGGTGCACGCTCTCAGGGAAAGA 1361
Db 1305 AAAAGATGTAACTACACCAAGATAGTGTAGACAGAGCCAGCCCTGGATGGGACTTT 1364
QY 1362 ATATCAGCTGTCTTACCTGGGACAGAGTGAACACTCCACCGGCTGTCGCAATGG 1421
Db 1365 CTACAGCTCATGTTATCATCAGACAGACCGGGAGCTCTGCATAAAGAGTATCTCTTAC 1424
QY 1422 AGCTCAGCTCAGTGTCTTTGGAGATCTGGCCTTTGTCCAGAACCAACAGCCGTTGAGAG 1481
Db 1425 AAAAGAGTGTGATCTCATCGAGGAGACCCCAACTCTTCCGGGACTTTGAAACCGTCTAAG 1484
QY 1482 CATG-----AAATGTACACAGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1529
Db 1485 TCTGTGTATCTCTCAAGAGGGGAGGAAGTTTGTCTATGAGGCTTCAACCTCTGGAGT 1544
QY 1530 GACAAAGTGAACACAGCAACTGTGGCGTCTCCAGAGCTGCTCGAGTGTATCTCTGCG 1589
Db 1545 GTTCCAGCGCCCTTGGCATTTCTGGAAAGACAGGAGTGTGAGAGTGTGTGTAGC 1604
QY 1590 CCAGGACCCCGTGTGCGCTGGAGCTTCCGGCTTGTGCTGTGTGTGGGCC 1639
Db 1605 ACGGGACCCCTACTGTGCTGGAGCCAGCCATCAAGGCTCTGTGTATCCC 1654

RESULT 12
PCT-US03-27411-44
; Sequence 44, Application PC/TUS0327411
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; Lee, Soo Yeun;
; APPLICANT: ELLIOTT, Vicki S.; HAFALIA, April J.A.;
; APPLICANT: BURFORD, Neil; SPRAGUE, William W.;
; APPLICANT: GRIFFIN, Jennifer A.; YANG, Yonghong G.;

782 GAGTGTGGACTCCTATGAGCGCATCAAGGTCCCAGAGTGGCCCG----- 827

; APPLICANT: GRIFFIN, Jennifer A.; YANG, Yonghong G.
; APPLICANT: CHAWLA, Narinder K.; BAUGHN, Mariah B.

APPLICANT: BECHA, Shanya D.; KHARE, Reena;
APPLICANT: THORNTON, Michael B.; MASON, Patricia M.;
APPLICANT: GIETZEN, Kimberly J.; ISON, Craig H.;
APPLICANT: MARQUIS, Joseph P.; SWARNAKAR, Anita;
APPLICANT: RAMKUMAR, Jayalaxmi; JIN, Pei;
APPLICANT: RICHARDSON, Thomas W.; TRAN, Uyen K.
TITLE OF INVENTION: NEUROTRANSMISSION-ASSOCIATED PROTEINS
FILE REFERENCE: PF-1557 PCT
CURRENT APPLICATION NUMBER: PCT/US03/27411
CURRENT FILING DATE: 2003-09-02
PRIOR APPLICATION NUMBER: US 60/408,383
PRIOR FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: US 60/408,781
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/414,221
PRIOR FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/426,483
PRIOR FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 60/431,566
PRIOR FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: US 60/434,317
PRIOR FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: US 60/437,763
PRIOR FILING DATE: 2003-01-03
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PERL Program
SEQ ID NO 40
LENGTH: 725
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: 7520844CB1
PCT-US03-27411-40

Query Match 6.2%; Score 145; DB 1; Length 725;
Best Local Similarity 73.1%; Pred. No. 1.2e-29;
Matches 302; Conservative 0; Mismatches 60; Indels 51; Gaps 7;
QY 151 CCCATCTCCGAGGCTGACTCTCTACCCGGGTTTCAGCGGTCTCATACGTTACATAATPAC 210
DB 273 CTCTGCTGAGAGGCTGACTCTCTGCTCACCCGGGTTTCGAGTCCCTCACACATACATPAC 332
QY 211 TCTGCTCTCTTGGGATCTTCCCTCCACACACTTACGTTCGGGTGACGGGATGACATC 270
DB 333 TCTGCTCTCTTGGGATCTTCCCTCCACACACTTATGTTGGGCGCCGGGACACCATC 392
QY 271 TTGCTTTTA-ACCCTCCCTCTCTGCGGAAGACCCCGAAGG----- 312
DB 393 TTGCTTTATCCCTGCCCCCTCTCAGGGGAGAGACCCCGAGGTTGAGAGACAAGAGAGG 452
QY 313 -----ATCGACTGGATGTGACTGAGACTCAGACAGAA 347
DB 453 GAACGGACCCCTGACCCTGTAGCATATTGACTGATGTTCTGAGGCTCAGACAGAA 512
QY 348 CTGAGGAG- AAGGCAAGAAAGAGGACGAATG-TCACAAATTTATCCAGATTC--TCG 403
DB 513 CTGTAGGAGAAAGGCAAGGACGACAGACGAATGTTCAACATTTGTCCAGATTCCTCGC 572
QY 404 CCATTGTCATGCTCTACCTCTCT- -CAGTTCGGGACCTTCGCTTTTATCGGAAGT 460
DB 573 CATTTGGCAATGCTCTCACTTCTCACTTGTGGCAACCTTTCGCTTTTATCGGAAGT 632
QY 461 GCGGGGTTATTGATGTGT-CCAGTTTCCAGCAGGTTGAAGACTTGAGAGCGG 512
DB 633 GCGGGTTATTGATGTGTGCCAGGTTCCAGAGGGTTCAACAGACTTGAGCAG 685

RESULT 14
PCT-US03-09929-21
Sequence 21, Application PC/TUS0309929
GENERAL INFORMATION:
APPLICANT: Curogen Corporation, et al.

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND MET
FILE REFERENCE: 21402-573B-061
CURRENT APPLICATION NUMBER: PCT/US03/09929
CURRENT FILING DATE: 2003-04-01
PRIOR APPLICATION NUMBER: 60/368,996
PRIOR FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/369,980
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 60/370,381
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/370,969
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: 60/371,002
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/372,002
PRIOR FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: 60/384,297
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: 60/386,816
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 60/389,123
PRIOR FILING DATE: 2002-06-13
PRIOR APPLICATION NUMBER: 60/402,207
PRIOR FILING DATE: 2002-08-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 179
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 21
LENGTH: 1327
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (2)..(1327)
PCT-US03-09929-21

Query Match 2.7%; Score 62; DB 1; Length 1327;
Best Local Similarity 47.6%; Pred. No. 1.2e-06;
Matches 280; Conservative 0; Mismatches 275; Indels 33; Gaps 2;
QY 332 AGACTCAGACAGAACTGCAGGAAGAAAGCAAGAGACCAATGTCACAATTTTA 391
DB 147 AGCCGATGTAGACACATGCAGAATGAAGGAAACATAAGATGAGTGCCACACTTTA 206
QY 392 TCCGATTTCTGCCATTTGTCAATGCTCTCACCTCTCACGTGCGGCACCTTCGCTTTG 451
DB 207 TTAAGTTCTCTAAGAAACAGATGATGATTTGTTCTGTGGAACATATGCTTCA 266
QY 452 ATCCGAAGTGGGGTTATTGATGTGTCAGTTTCCAGAGGTTGAAAGACTTGAGAGCG 511
DB 267 ACCCTTCTCGAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGCG 326
QY 512 GCGGGGAAATGCTCTTTTGAGCCAGCTCAACGTCAGCAGCTGTAATGGTGGGGGG 571
DB 327 GAATGGCCAGATGCCCATATGATGCCAACATGCCAAGCTTGCACATGTTGAGATGGA 386
QY 572 TCCTCTACCGCCACTGTGAAGAACTTCCTGGGACTGAGCCCATCATCTCCCGAGCTG 631
DB 387 AACTATACAGCCACAGTACTGACTTCTTCCCTTGGCCATTTGACCGACTCATTTACCGAGTC 446
QY 632 TGGGTCGAGCTGAGGACTGGATTTCGAACAGAGACCTTGTCACTTCCTGGCTTAATGCTCCAG 691
DB 447 TTGGAGAAAGCCCTACCCCTGCGGACCGCTCAAGCAGCATTTCAAAATGGTTGAAAGAACCAT 506
QY 692 CTTTGTCCGAGCTATGTTCTTGACCCAGCTGAGTGGGGGATGAACATGGAGACGATG 751
DB 507 ACTTTGTTCAAGCCGTG-----GATTACGGAGATT 536
QY 752 AAATCTTTTTTTTCTTACGGAGACCTCCCGAGTGTGGAGCTTCTTATGAGCGCATCAAGG 811
DB 537 ATATCTACTTCTTCTTACGGGAAATAGCAGTGGAGTATACACCATGGGAAGAGTAGTTT 596
QY 812 TCCCAAGAGTGGCCCGAGTGTGTGCGGGGAGCTTTGGGGGAGGAGAACCCCTTTCAGCAGA 871

Db 597 TCCCAAGAGTGGCTCAGGTTTGAAGATGATATGGAGGATCTCAAGAGTCTCTGGAGA 656
QY 872 GA---TGGACGACGTTTCTGAAGGCTGACCTGCTGTGCCCGAGGCCG 916
Db 657 AACAGTGGACGTCGTTCTCTGAAGGCGCGCTTGAAGTGTCTCAGTTCTG 704

RESULT 15

PCT-US03-17412-21

; Sequence 21, Application PC/TUS0317412

; GENERAL INFORMATION:

; APPLICANT: Curagen Corporation

; APPLICANT: Alvarez, Enrique

; APPLICANT: Anderson, David W.

; APPLICANT: Dhanabal, Mohanraj

; APPLICANT: Khrantsov, Nikolai V.

; APPLICANT: Larocheville, William J.

; APPLICANT: Li, Li

; APPLICANT: Lichenstein, Henri

; APPLICANT: Ooi, Chean Eng

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Shinkets, Richard A.

; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME

; FILE REFERENCE: 15966-540CIP2

; CURRENT APPLICATION NUMBER: PCT/US03/17412

; CURRENT FILING DATE: 2003-05-30

; PRIOR APPLICATION NUMBER: 09/520,781

; PRIOR FILING DATE: 2000-03-03

; PRIOR APPLICATION NUMBER: 60/123,667

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: 60/234,082

; PRIOR FILING DATE: 2000-09-20

; PRIOR APPLICATION NUMBER: 60/233,798

; PRIOR FILING DATE: 2000-09-19

; PRIOR APPLICATION NUMBER: 60/174,485

; PRIOR FILING DATE: 2000-01-04

; PRIOR APPLICATION NUMBER: 10/403,676

; PRIOR FILING DATE: 2003-03-31

; PRIOR APPLICATION NUMBER: 60/371,002

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/384,798

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: 60/402,407

; PRIOR FILING DATE: 2002-08-09

; PRIOR APPLICATION NUMBER: 60/443,062

; PRIOR FILING DATE: 2003-01-28

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: CuraSeqList version 0.1

; SEQ ID NO 21

; LENGTH: 1327

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (2)..(1327)

PCT-US03-17412-21

Query Match 2.7%; Score 62; DB 1; Length 1327;
Best Local Similarity 47.6%; Pred. No. 1.2e-06;
Matches 280; Conservative 0; Mismatches 275; Indels 33; Gaps 2;

QY 332 AGACTCACAGACAGAACTGCGAGGAAGAGGCAAGAGGACCAATGTCTACAAATTTTA 391
Db 147 AGCGCGATGTAGACACATGCAGATGAAGGGAACACATAAGGATGAGTCCCAACTTTA 206
QY 392 TCCAGATTCTGCCCAATGTCAATGCCTCTCACCTCTCACGTGCGGACCCCTTCGCTTTTG 451
Db 207 TTAAGTCTCTTAAGAAAGAAACGATGATGCATTGTTGCTGTGGAACATAATGCCTTCA 266
QY 452 ATCCGAAGTGGGGGTTATTGATGTCTCAGTTCCAGCAGGTTTCAAGACTTTGAGAGCG 511

Db 267 ACCCTTCTCTGCAGAAACTATAAGATGGATACATTGGAACCAATTCGGGGATGAATTCAGCG 326
QY 512 GCCGGGGAAATGTCTCTTTTGGAGCCAGCTCAACGGTCAAGAGTGTAAATGGCTGGGGCG 571
Db 327 GAATGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACCTGTTTGCAGATGGAA 386
QY 572 TCCTCTACACCGCCACTGTGAAGAACTCTCTGGGACTGAGCCCATCATCTCCCGAGCTG 631
Db 387 AACTATACTCAGCCACAGTGAAGTCTCTTGGCCATTGACGACGATCATTTACCGGAGTC 446
QY 632 TGGTCCGAGCTGAGGACTGGATTTCGAACAGAGACCTTGTCTATCTCTCCCTGCTTAATGCTCCAG 691
Db 447 TTGGAGAAAGCCCTTACCTCGCGACCGTCAAGCAGCATTTCAAAATGGTTGAAGAACCAT 506
QY 692 CCTTTGTGCGCAGCTATGCTCTGAGCCAGCTGAGTGGGGGATGAAGATGGAGACGATG 751
Db 507 ACTTTGTTCAAGCCGTG-----GATTACGGAGATT 536
QY 752 AAATCTTTTTTTTCTACGGAGACCTCCCGAGTGTGGACTCTCTATGAGCCCATCAAGG 811
Db 537 ATATCTACTTCTTCTCAGGGAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTT 596
QY 812 TCCCAAGAGTGGCCCGAGTGTGTCGGGGGACCTTGGGGGAGGAGAGACCCCTTCAGCAGA 871
Db 597 TCCCAAGAGTGGCTCAGGTTTGTAAAGATGATATGGGAGGATCTCAAGAGAGTCTCGAGA 656
QY 872 GA---TGGACGACGCTTCTGAAGGCTGACCTGTGTGCCCGAGGCCG 916
Db 657 AACAGTGGACGTCGTTCTCTGAAGGCGCGCTTGAAGTGTCTCAGTTCTG 704

Search completed: September 26, 2003, 11:35:56

Job time : 365.737 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 25, 2003, 19:18:34 ; Search time 4613.83 Seconds
(without alignments)
12279.116 Million cell updates/sec

Title: US-09-284-180a-2

Perfect score: 2331

Sequence: 1 atgttgccaggccgagcg.....gtgatgagacctcatctaa 2331

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1515	65.0	2719	11 AK035993	AK035993 Mus muscu
2	1511.8	64.9	2855	11 AK047067	AK047067 Mus muscu
3	645	27.7	704	14 CB527136	CB527136 UI-M-FY0-
4	632.6	27.1	691	12 BM944530	BM944530 UI-M-EH0p

5	608	26.1	868	10	BG3323723	BG3323723
6	596.4	25.6	693	12	BM963828	BM963828
7	586.2	25.1	901	13	BQ213659	BQ213659 AGENCOURT
8	560	24.0	1154	12	BM462308	BM462308 AGENCOURT
9	557.6	23.9	733	10	AW953466	AW953466 EST165536
10	547.8	23.5	765	12	BI823626	BI823626 603038515
11	546.8	23.2	701	10	AW957134	AW957134 EST369204
12	540	23.5	733	14	CB245456	CB245456 UI-M-FY0-
13	508.8	21.8	772	12	BI915256	BI915256 603184795
14	496	21.3	758	14	CB244307	CB244307 UI-M-FY0-
15	484	20.8	669	10	BB628682	BB628682 BB628682
16	475.6	20.4	578	12	BI344452	BI344452 372924 MA
17	464.2	19.9	669	12	BE774505	BE774505 602662571
18	455.6	19.5	486	10	BE982860	BE982860 UI-M-CG0p
19	437.2	18.8	466	9	AW123399	AW123399 UI-M-BH2
20	405.2	17.4	434	9	AW123577	AW123577 UI-M-BH2
21	397.4	17.0	556	10	BE683223	BE683223 182687 MA
22	393	16.9	444	13	BY230889	BY230889 BY230889
23	386.8	16.6	503	9	AA459837	AA459837 2x50g12.r
24	381.2	16.4	1045	10	BE734978	BE734978 601570573
25	380	16.3	380	14	CB810579	CB810579 AMGNNUC:Y
26	375.2	16.1	522	10	BE667719	BE667719 155505 MA
27	366.4	15.7	368	10	BF415905	BF415905 UI-R-CA0-
28	363.8	15.6	466	12	BI275275	BI275275 UI-R-CA0-
29	352.2	15.1	416	13	BY224521	BY224521 BY224521
30	346.6	14.9	396	13	BY203844	BY203844 BY203844
31	340	14.6	616	14	BY731493	BY731493 BY731493
32	333	14.3	769	13	BQ745165	BQ745165 UI-M-EH0p
33	314.2	13.5	361	13	BY192163	BY192163 BY192163
34	312	13.4	430	13	BY225500	BY225500 BY225500
35	308.8	13.2	354	13	BY176252	BY176252 BY176252
36	304.2	13.1	426	10	BE754071	BE754071 207388 MA
37	303.4	13.0	365	14	CD355327	CD355327 UI-M-FY0-
38	296.2	12.7	343	13	BY186478	BY186478 BY186478
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44	284.4	12.2	376	9	AW436751	AW436751 77209 MAR
45	283.8	12.2	437	14	H24181	H24181 ym55f02.r1

ALIGNMENTS

RESULT 1
LOCUS AK035993 2719 bp mRNA linear HTC 05-DEC-2002
DEFINITION Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:9630025H20 product:sema domain, immunoglobulin domain (Ig), TM domain, and short cytoplasmic domain, full insert sequence.

ACCESSION AK035993
VERSION AK035993.1 GI:26084949
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
1 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
2 99279253
PUBMED 10349636

REFERENCE
1 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
20499374

Qy	778	TCCCGAGTGTGGACTCCTATGAGCGCATCAAGGTCCCAAGAGTGGCCGAGTGTGTCG	837	ORGANISM	Mus musculus
Db	891	TCCCGAGTGTGGACTCATATGAGCGCATCAAGGTCCCAAGAGTGGCCGAGTGTGTCG	950	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
Qy	838	GGGACCTTGGGGCCGAGAGACCTTCAGCAGAGATGGACGAGTTTCTGAAGCTGAC	897	AUTHORS	Carninci, P. and Hayashizaki, Y.
Db	951	GGGGCCCTTGGGGCCGAGAGACCTTCAGCAGAGATGGACGAGTTTCTAAAGGCTGAC	1010	TITLE	High-efficiency full-length cDNA cloning
Qy	898	CTGCTGTGCCAGGGCCGAGCATGGCGGCTCCCGGCTTCGAGGCTATGGCAGAG	957	JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
Db	1011	CTGCTGTGCCAGGGCCGAGCATGGAGGCTTCGGGTTCTGCAGGATATGACAGAG	1070	MEDLINE	99279253
Qy	958	CTTGCGCTCAGCTGAGCGGGAACCCCATCTTTTATGGGATCTTTCTCCCTCCAGTGG	1017	PUBMED	10349636
Db	1071	CTTCGACCTCAGCTGAGCGGGAACCCCATCTTTTATGGGATCTTTCTCCCTCCAGTGG	1130	REFERENCE	2
Qy	1018	GAAGGAGCTGCCATCTCTGCTGTGTGTGCTTCGAGCCCAAGACATCCGGGAGTGGT	1077	AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Sugahara, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Db	1131	GAAGGAGCTGCCATCTCTGCTGTGTGTGCTTCGAGCCCAAGACATCCGGGAGTGGT	1190	TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Qy	1078	AATGGTCCCTTTAGAGAGCTAAACATGACTGCAACAGGGGACTGCTGTCATGGACAAC	1137	JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
Db	1191	AATGGTCCCTTTAGAGAGCTAAACATGACTGCAACAGGGGACTGCTGTCATGGACAAC	1250	MEDLINE	20499374
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Db	1251	GAGTGCCCGCAGCCAGCCTGGAGAGTGCATGCCCAACATGAAGCTCCAGCAGTTT	1310	REFERENCE	3
Qy	1198	GGATCCTCACTCTCCCTGCCAGACCGCGTGTCTACCTTTATCAGAGACCCCTCTCATG	1257	AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, M., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
Db	1311	GGATCCTCACTCTCCCTGCCAGACCGCGTGTCTACCTTTATCAGAGACCCCTCTCATG	1370	TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
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Qy	1318	CTCAGATCTGCGCCACAGGGTGACAGCCTCTCAGGGAAGAAATATGACGTGCTCTAC	1377	PUBMED	11076861
Db	1431	CTCAGATCTGCGCCACAGGGTGACAGCCTCTCAGGGAAGAAATATGACGTGCTCTAC	1490	REFERENCE	4
Qy	1378	CTGGGGACAGAGGATGACACCTCCACCGGCTGTGGCATTTGAGCTCAGCTCAGTGC	1437	AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaoka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Stauble, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kaniyama, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
Db	1491	CTGGGGACAGAGGATGACACCTCCACCGGCTGTGGCATTTGAGCTCAGCTCAGTGC	1550	TITLE	Functional annotation of a full-length mouse cDNA collection
Qy	1438	TTGGAGGATCTGGCTTTGTTCCAGAACACAGCCGCTTGAGAGCATGAATTTGACCAAC	1497	JOURNAL	Nature 409 (6821), 685-690 (2001)
Db	1551	CTGGAGGATCTGGCTTTGTTCCAGAACACAGCCGCTTGAGAGCATGAATTTGACCAAC	1610	MEDLINE	21085660
Qy	1498	GATTGGCTCTGGTGGCTCCCATCTAGGTGACACAAAGTGAACACAGCAACTGTGGC	1557	PUBMED	11217851
Db	1611	GATTGGCTCTGGTGGCTCCCATCTAGGTGACACAAAGTGAACACAGCAACTGTGGC	1670	REFERENCE	5
Qy	1558	CGTCTCCAGAGCTCTCGAGTGTATCTTGGCCAGGACCCCGTGGCTGAGCTTC	1617	AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Db	1671	CGTCTCCAGAGCTCTCGAGTGTATCTTGGCCAGGACCCCGTGGCTGAGCTTC	1730	TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Qy	1618	CGGCTTGATCTGTGTGGCCAGCGCGGAGCACCGCGGATGGT	1664	JOURNAL	Nature 420, 563-573 (2002)
Db	1731	CGGCTTGATCTGTGTGGCCAGCGCGGAGCACCGCGGATGGT	1777	MEDLINE	6 (bases 1 to 2855)
RESULT 2	AK047067	2855 bp	linear	HTC 05-DEC-2002	
LOCUS	Mus musculus	10 days neonate cerebellum cDNA, RIKEN full-length			
DEFINITION	enriched library, clone:B930015409 product:sena domain, immunoglobulin domain (Ig), TM domain, and short cytoplasmic domain, full insert sequence.				
ACCESSION	AK047067				
VERSION	AK047067.1	GI:26091917			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				


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/notes="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCCAGGAC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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BASE COUNT 145 a 177 c 207 g 161 t 1 others

Query Match 27.1%; Score 632.6; DB 12; Length 691;
Best Local Similarity 95.5%; Pred. No. 1e-149;
Matches 661; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

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QY 378 ATGTACAAATTTATCCAGATTCGCGCAATGTGAATGCCCTCACCTCCACGTGGG 437
DB 61 ATGTACAAATTTATCCAGATTCGCGCAATGTGAATGCCCTCACCTCCACGTGGG 120

QY 438 CACCTTCGCTTTGATCCGAAGTGGGGGTTATTGATGTGCCAGTTTCCAGCAGGTGA 497
DB 121 CACCTTCGCTTTGATCCGAAGTGGGGGTTATTGATGTGCCAGTTTCCAGCAGGTGA 180

QY 498 AAGACTTCAGAGCGCGCGGGAATGTCCTTTGAGCCAGCTCAACGGTCAGCAGCTGT 557
DB 181 AAGACTTCAGAGTGGCGGGGAATGTCCTTTGAGCCAGCTCAACGGTCAGCAGCTGT 240

QY 558 AATGGCTGGGGCGCTCTTACACCGCCACGTGTGAAGAACTTCTCTGGGACTGAGCCCAT 617
DB 241 AATGGCTGGGGCGCTCTTACACCGCCACGTGTGAAGAACTTCTCTGGGACAGCCGAT 300

QY 618 CATCTCCGAGCTGTGGGTGAGCTGAGGACTGGATTGCGAACAGAGACCTTTGTCATCTG 677
DB 301 TATCTCCGAGCTGTGGGTGAGCTGAGGACTGGATTGCGAACAGAGACCTTTGTCATCTG 360

QY 678 GCTTAATCTCCAGCCTTTGCGAGCTATGGTCTGAGCCAGCTGAGTGGGGGATGA 737
DB 361 GCTTAATCTCCAGCCTTTGCGAGCTATGGTCTGAGCCGCTGAGTGGGGGATGA 420

QY 738 AGATGGAGACGATGAATCTTTTCTTTCACGAGACCTTCCGAGTGTGGACTCTGA 797
DB 421 AGATGGAGACGATGAATCTTTTCTTTCACGAGACCTTCCGAGTGTGGACTCTGA 480

QY 798 TGAGCGGATCAAGTCCCAAGATGGCCCGAGTGTGTGCGGGGACCTTGGGGGACGAA 857
DB 481 TGAGCGGATCAAGTCCCAAGATGGCCCGAGTGTGTGCGGGGACCTTGGGGGACGAA 540

QY 858 GACCTTCAGCAGAGATGGAGCAGCTTCTCAAGCTGACCTGCTGCTCCAGCGCCGA 917
DB 541 GACCTTCAGCAGAGATGGAGCAGCTTCTCAAGCTGACCTGCTGCTGCTCCAGCGCCGA 600

QY 918 GCATGGCGCGCCCGGGTTCTGACAGCTATGGCAGAGCTTCGGGCTCAGCCTGGAGC 977
DB 601 GCATGGAGGCGCCCGGGTTCTGACAGATATGACAGAGCTTCGACCTTCAGCCTGGCGC 660

QY 978 GGGAAACCCCATCTTTTATGGGATCTTTTCCT 1009
DB 661 GGGGACCCCT-TCITTTATGGCATCTTTTCCT 691

RESULT 5
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LOCUS 602421820F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4560028 5',
DEFINITION mRNA sequence.

ACCESSION BG323723
VERSION BG323723.1 GI:13130160
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 868)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LUCM1268 row: g column: 05
High quality sequence stop: 860.

FEATURES
Location/Qualifiers
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EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 167 a 240 c 273 g .188 t

ORIGIN
Query Match 26.1%; Score 608; DB 10; Length 868;
Best Local Similarity 84.0%; Pred. No. 2e-143;
Matches 712; Conservative 0; Mismatches 130; Indels 6; Gaps 2;

QY 1484 TGAATTGTACACGATTGGCTCTCTGGTGGCTCCCATCTAGGTGACACAGTGAACA 1543
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QY 1544 CCAGCAACTGTGGCGCTCTCCAGAGCTGCTCGGAGTGTATCTTGGCCAGGACCCGCTGT 1603
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QY 1604 GCGCTTGAGCTTCGGGCTTGTGTTGGCCAGCGGAGCACCAGCGGATGG 1663
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QY 1664 TTCAAGATATAGTTCAGCGGATGTCTCTTTTGTGTCCAAAAGCACTGGAGAACATC 1723
DB 182 TCCAAGACATAGTTCAGCAGATGTCTCTCTTTGTGTCTTAAAGAGCCTGGAGAACGTC 241

QY 1724 CCGTAGTGTGTTGAAGTTCGGGTGGCTACTGTGGGCCAGCTGGTCTGCATGTTCCCCCA 1783


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||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
600 GCAGCGCGCGGACAGAGGGAGCTTCTAGCTAGAGACAAGTGGGCTTAGATCTGGGGG 659

2130 TCCACCTCTCTGGGACCAACAGCTATAGTCAGGAC 2163
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
660 CTCACCTCTCTGGGACCAACAGCTATAGCCAAGAC 693

RESULT 7
LOCUS      BQ213659
DEFINITION AGENCOURT_7595087 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6062683
5', mRNA sequence.
ACCESSION  BQ213659
VERSION     BQ213659.1 GI:20395053
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished
            Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13334 row: 1 column: 20
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                Average insert size 2 kb. Library constructed by Life
                Technologies."
BASE COUNT  181 a 248 c 289 g 183 t
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Query Match      25.1%; Score 586.2; DB 13; Length 901;
Best Local Similarity 86.3%; Pred. No. 7e-138;
Matches 648; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

1283 GCGCGCCCTCTGCTGCTACTACAGATACAGCTATCTCAGTCTGCGGCCACAGGGTCA 1342
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
12  GGCACCCCTCTGCTGCTACTACAGATACAGCTATCTCAGTCTGCGGCCACAGGGTCA 71
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1343 CCAGCCTCTCAGGGAAGAAATATACGCTCTACCTGGGGACAGAGGATGGACACCTCC 1402
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
72  CCAGCCTCTCAGGGAAGAAATATATGCTCTACCTGGGGACAGAGGATGGACACCTCC 131
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1403 ACCGGCTCTGCGCATTTGGAGCTCAGCTCAGTCTCTTGGAGGATCTGGCTTGTTCACAG 1462
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
132 ACCGAGCAGTGGGATCGGAGCTCAGCTCAGCTCAGCTGCTTGAAGATCTGGCTTATTCACAG 191
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1463 AACACAGCGGTTTGAGAGCATGAATTTACACGATTTGGCTCTCTGTTGGGCTCCCAT 1522
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
192 AGCCACAGCCATTGAGACATGAATTTGACACAGCTGGCTCTCTGTTGGCTCCCGTA 251
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1523 CTGAGGTGACAACTGACACCACTGCTGGCCGCTCTCCAGAGCTGCTCGGAGTGA 1582
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Db      252 CTGAGGTGACACAAAGTGAATACAAACCACTGTGGCCGCTTCCACAGAGTGTCTCAGAGTGCA 311
Qy      1583 TCCTGGCCCCAGGACCCCGTGTGGCCCTGGAGCTTCCCGCTTGATGCTGTGTGGCCCAAG 1642
Db      312 TCCTGGCCCCAGGACCCAGTCTGTGCTGGAGCTTCCGCTGGATGAGTGTGTGGCCCATG 371
Qy      1643 CCGCGAGACCGCGGGATGTTCAAGATATAGAGTACAGCGGATGTCTCTCTTTGTGTCTC 1702
Db      372 CCGGGGAGCACCGAGGGTTGGTCCAGACATAGAGTCAGAGATGTCTCCTCTTTGTGTCTC 431
Qy      1703 CAAAAGAACCTGGAGAACATCCCGTAGCTGTTTGAAGTTCGGTGGCTACTGTGGGCCACG 1762
Db      432 CTAAGAGACCTGGAGAACGTCACAGTAGTGTGAAGTTCCGCTGGCTACAGCTGCGCATG 491
Qy      1763 TGGTCTCTGCCATGTTCCGCCAGTTCTGCCTGGGCATCTGTGTGTGGCACAGCCCAAGTG 1822
Db      492 TGGCTCTGCCATGTTCTCCAAAGCTCAGCATGGGCATCTGTGTGTGGCACAGCCCAAGTG 551
Qy      1823 GAGTGAAGTGGCTACTTCCCGGAGGATGAGTATAGAGTGGTGGTGACCCCAAGGGGCCA 1882
Db      552 GAGTGAAGTGGCTACTTCCCGGAGGATGAGTATAGAGTGGTGGTGACCCCAAGGGGCCA 611
Qy      1883 TGGGGGCTTATGCTTGGAGTGTGAGAGGTTGAGAGGTTGGGGCAGCCCATGTGGTAGCAGCTTACA 1942
Db      612 TGGGGGCTTATGCTTGGAGTGTGAGAGGTTGAGAGGTTGGGGCAGCCCATGTGGTAGCAGCTTACA 671
Qy      1943 GCTTGGTGGGGCAGCAGCGGGGACCTCAAAACCGGGGCCACACCGTTGTGGGGGCTG 2002
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Qy      2003 GATTGTTGGCTTCTCTCTGGGTGTTCTTTCG 2033
Db      732 ACTGGCTGGGCTTCTTCTGGGGGATTCCTCC 762

RESULT 8
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DEFINITION AGENCOURT_6424556 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5491453
5', mRNA sequence.
ACCESSION  BM462308
VERSION     BM462308.1 GI:18511348
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished
            Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12111 row: p column: 14
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FEATURES
source

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BASE COUNT	Average insert size 1.75 kb.		Library constructed by Life
ORIGIN	Technologies."		
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Best Local Similarity	84.4%	Pred. No. 3.5e-131;		
Matches 648;	Conservative 0;	Mismatches 105;	Indels 15;	Gaps 1;

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DB			
QY	61	CCGCGCGCGCTGCTGCTGCTGCTGCTGGCGATACTAAGCCGCCCGGCTGCGGCGCG	120
DB			
QY	146	CC-----GCTACTGCTGCTGGCGGTGCTGAGCGGCCGGTATCGGCGCG	190
DB			
QY	121	GTCCCGGCTCAGTGCCAGAACCTCGCTGCCCATCTCGAGGCTGACTCTATCTAACC	180
DB			
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DB			
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DB			
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DB			
QY	241	ACACTTTACGTCGGTGCCACGGATAGCATCTTCGCTTTTAAACCTTCCCTTCTCTGGGAA	300
DB			
QY	311	ACACTTTATTTGGCGCCGGGACACATCTTCGCTTTATCCCTGCGCTTCTCAGGGAG	370
DB			
QY	301	AGACCCCGAAGGATCAGCTGGATGGTACCTGAGACTCACAGACAGAACTCGACGAGAAA	360
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QY	371	AGACCCCGCAGGATCTACTGGATGGTTCCTCGAGGCTCACAGACAGAACTGTAGGAGAAA	430
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QY	361	GGCAAGAAAGAGACGAATCTCAAAATTTATCCAGATTCGCGCAATGTCAATGGCTCT	420
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QY	431	GGCAAGAAAGAGACGAATGTCAAAATTTGTCTCAGATTCGCGCAATGGCAATGGCTCT	490
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QY	421	CACCTCCTCAGCTGCGGCACCTTCCTGCTTTTGTATCCGAAGTCGCGGGTTATGTATGTCC	480
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QY	481	AGTTTCCAGCAGCTTGAAGACTTGAGCGCGCGGGGGAATGTCTTTTGAGCCAGCT	540
DB			
QY	551	AGTTTCCAGCAGCTTGAAGACTTGAGGTGGCGGGGAAATGTCTTTTGAGCCAGCT	610
DB			
QY	541	CAACGGTCAACAGCTGTAAATGGCTGGGGCGCTCTACACCGCCACTGTGAAGAACTTC	600
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QY	671	CTGGGACGAGGCAATATCACAGACAGTGGGTCGTGCCGAGGACTGGATTCGGACA	730
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QY	731	GATACCTTGCTTCTCTGGCTGAACGCCCGAGCCTTTGTGCGACCGGTGGCTTGAACCCA	790
DB			
QY	721	GCTGAGTGGGGATGAAGATGGAGCATGAATCTTTTTTCTTC	768
DB			
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DB			

RESULT 9	AW953466	733 bp	mRNA	linear	EST 01-JUN-2000
LOCUS	AW953466				
DEFINITION	EST355536 MAGE resequences, MAGB Homo sapiens cDNA, mRNA sequence.				
ACCESSION	AW953466				
VERSION	AW953466.1	GI:8143149			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				

REFERENCE	1 (bases 1 to 733)
AUTHORS	Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.
TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
JOURNAL	Unpublished
COMMENT	Contact: John Quackenbush The Institute for Genomic 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: johnq@tigr.org Plate: 51
FEATURES	Seq primer: Reverse.
source	1. .733 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone_lib="MAGE resources, MAGEB" /note="Vector: pBluescriptSkM"
BASE COUNT	133 a 207 c 238 g 154 t
ORIGIN	1 others

Query Match	23.9%	Score 557.6	DB 10	Length 733
Best Local Similarity	86.5%	Pred. No. 1.2e-130		
Matches 627	Conservative 0	Mismatches 95	Indels 3	Gaps 1
QY	1485	GAATTTGTACCAAGATTGGCTCTCTGGTGGGCTCCCATACTAGGTGACACAAGTGAACAC	1544	
Db	11	GAATTTGTACCAAGCTGGCTCTGGTGGTCTCCCGTACTGAGGTGACACAAGTGAATAC	70	
QY	1545	CAGCAACTGTGGCGCTCTCCAGAGCTGCTCGGAGTGTATCTGCGCCAGGACCCCGTGTG	1604	
Db	71	AACCAACTGTGGCGGTCTCAGAGCTGCTCAGAGTGCATCTTGCCCGAGACCAAGTCTG	130	
QY	1605	CGCTTGAGGCTTCCGGCTTGATCTTGTGTGGCCCAAGCCGGGAGACACCGCGGATGGT	1664	
Db	131	TGCTTGAGCTTCCGGCTTGATGAGTGTGTGGCCATGCGGGGAGCACCGAGGGTTGGT	190	
QY	1665	TCAAGATATAGACTACGGGATGTCCTCTTCTTGTCTCAAAGAAGACCTCGAGACAATCC	1724	
Db	191	CCAAGACATAGATGACAGATGCTCCTCTTTGTCTCTAAAGAGCCTCGAGAACGTCC	250	
QY	1725	CGTAGTGTTTGAAGTTCCCGTGGCTACTGTGGCCACAGTGTCTCGCATGTTTCCCCCGAG	1784	
Db	251	AGTAGTGTTTGAAGTTCCCGTGGCTACAGCTGGCATGTGGTCTTGGCATGTTTCTCCAG	310	
QY	1785	TTCTGCGTGGGCATCTGTGTGGCACCAAGCCAGTGGAGTGAAGTCTGCTCTCACTCCCGG	1844	
Db	311	CTCAGCATGGCATCCTGTGTGTGGCACCAAGCCAGTGGAGTGAAGTCTCACTACCCCGG	370	
QY	1845	GAGGGATGGAAGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG	1904	
Db	371	GCGGGATGGAAGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG	430	
QY	1905	TCAGGAGGTGTGAGCGCCCGCTGGTGGTGTCTTATAGCTTGGTGTGGGGCAGCCAGCG	1964	
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QY	1965	GGAGACCTCAAAACGGGGCCACACCGTTGTGGGGGTGGATGGTGGCTTTCTCTCTGGG	2024	
Db	491	AGATGCTCCGAGCGGGGCCACAC---	547	
QY	2025	TGTTCTTGACAGTCCCTCACT	2084	
Db	548	GATTTCTCGAGCATCCTGACT	607	
QY	2085	GAGGAGCTTCTAGCTAGAGACAAGTGGGCTTAGATCTGGGGGCTCCACCTTCTGGGAC	2144	
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DB	11	GAATTTGTATCCACAGCTGGCTCTCGTGGTGGCTCCCGTACTAGGTGACAAAGTGAATAC	70						
QY	1545	CACCAACTGGCGCGTCTCCAGAGCTGCTCGGAGTGTATCCTGGCCAGAGACCCCGTGTG	1604						
DB	71	AACCAACTGGCGCGTCTCCAGAGCTGCTCAGAGTGCATCTGCGCCAGGACCCAGTCTG	130						
QY	1605	CGCTCGAGCTTCCGGCTTGACTGTTGTGTGGCCACAGCGCGGAGGACACCGCGGATGGT	1664						
DB	131	TGCTCGAGCTTCCGGCTGGATGAGTGTGTGGCCCATGCGCGGAGCACCGAGGTTGGT	190						
QY	1665	TCAGATATAGACTCAGCGGATGCTCTTTTGTGTCCAAAAGAACTCGAGAACATCC	1724						
DB	191	CCAAGACATAGACTCAGCAGATGCTCCTCTTTGTGTCTTAAAGAGCCTGAGAACGTCC	250						
QY	1725	CGTAGTGTTTCAAGTTCCCGTGGCTACTGTGGGCACAGTGGTCTGCATGTTCCCCCGAG	1784						
DB	251	AGTAGTGTTTGAAGTTCCCGTGGCTACAGCTGGCGCATGTGCTTGGCATGTTCTCCAAG	310						
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DB	311	CTCAGCATGGGCATCTGTGTGTGGCACACAGCCAGTGGAGTGACTGCATCACTCCCGCG	370						
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QY	1905	TCAGGAGGTGGAGCGCCCGCTGGTGGCTGCTTATAGCTTGGTGTGGGCGACGCCAGCG	1964						
DB	431	TCAGGAGGTGGGGCAGCCCATGTGTGTAGCAGCTTACAGCTTGGTATGGGGCAGCCAGCG	490						
QY	1965	GGACCCCTCAAAACCGGGCCACACCGTTGTGGGGCTGGATTGGTTGGCTTTCTCTCTGGG	2024						
DB	491	AGATGCTCCGAGCGGGGCCACAC--AGTGGGGCGGAGCTGGCTGGCTTCTCTTGGG	547						
QY	2025	TGTTCTTGACGATCCCTCACTCTCTCTCTGATTGTGTGCGCTCAGACAGCTCGGCGACA	2084						
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DB	608	GAAGGAACCTTCTGGCTAGAGACAAGTGGGCTTGGACCTGGGGGCTCCACCTTCTGGGAC	667						
QY	2145	CACAAGCTATAGTCAGGACCCCTCCCTCTCTCTCGCTGAAGATGAACGGCTGCCCTGGC	2204						
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QY	2205	CCTGGG	2210						
DB	728	CCCTGG	733						

RESULT 12	CB245456	701 bp	mRNA	linear	EST 12-FEB-2003
LOCUS	CB245456				
DEFINITION	UI-M-FYO-cdt-e-17-0-UI.r1 NTH_BMAP_FYO Mus musculus cDNA clone				
	IMAGE: 5834138 5', mRNA sequence.				
ACCESSION	CB245456				
VERSION	CB245456.1	GI:28367100			
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1
2
3
4
5
6
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Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae; Murinae; Mus.
1 (bases 1 to 701)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

The following repetitive elements were found in this cDNA sequence: 116-149, >GC-rich<low_complexity 166-207, >(CAG)_n<Simple_repeat (matched complement)
Seq primer: pVX-5.

FEATURES
SOURCE

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  /note="Organ: Brain; Vector: pYX- Asc; Site_1: Ecor I;
  Site_2: Not I; The library was constructed according
  to Bernaldo, Lennon and Soares, Genome Research, 6:791-806,
  1996. Denatured RNA was size fractionated on a 1% agarose
  gel. First strand cDNA synthesis was primed with oligo-dT
  primer containing a Not I site. Double strand cDNA was
  size selected according to mRNA size fraction, ligated
  with Ecor I adaptor, digested with NotI and then cloned
  directionally into pYX-Asc vector. The library tag
  sequence located between the Not I site and the polyA tail
  is AGGAGACAG. This library was created for the University of
  Iowa Brain Anatomy Project (BNAP): 'Gene Discovery in the
  Developing Mouse Nervous System', supported by National
  Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
  program coordinator."
  230 c 205 g 143 t

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Program Coordinator.			
BASE COUNT	123 a	230 c	205 g
ORIGIN	143 t		

Query Match	23.28	Score	540	DB	14	Length	701
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						Gaps	1

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Qy		178	ACCGGTTTGCAGGCTCTCATACGTAACAATTACTGCTCTCTTGTCGATCCTGCCCTCC	237
Db		286	ACCGGTTTGGGGCCCTCATACGTACAAATTACTGCTCTCTGCTGGATCCTGCTTCT	345
Qy		238	CACACACTTATCGTCGGTGACGGGATAGCATCTTCGCTTTAAACCTCCCCCTTCTGGG	297
Db		346	CACACATTATCGTCGGTGACGGGACAGCATCTTCGCTTTAAACCTGCCCTTCTTCTGGG	405

